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# **Flock Testing Feasibility Study**

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FLOCK TESTING FEASIBILITY STUDY

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Summary

The biodynamics of poultry health is a function of a complex set of events and interactions between the host (poultry), disease causing agents and environmental factors. In today's poultry industry, although the presence or level of many infectious agents have been reduced and birds are kept in relatively controlled environments, spatial and temporal differences in managerial and environmental factors affect the prevalence rates of diseases amongst farms. This also leads to subsequent differences in condemnation rates at the time of processing. Since the birds' genetic potential and environmental determinants are closely monitored to attain maximal growth with minimal losses due to diseases, the condition of birds in a flock tends to be homogeneous. It may then be possible to determine the health status of such a population of birds by examining the performance records and other possible indicators of health and by inspecting a representative sample from the flock before slaughtering the entire flock. Amongst the important health status indicators are such factors as strain of birds, hatchery management, types of brooding and housing, sanitation, vaccination, medications, feed utilization, morbidity and mortality, macro and micro climate and carcass inspection procedures. Each of these affect condemnation rates due to diseases either directly or indirectly. If the variables which are causally related to condemnation rate could be identified and their significance quantified, then one could device appropriate mechanisms to monitor the condemnation rate due to diseases and use it as an adjunct to existing carcass inspection procedures.



In recent years, inflation and the poultry industry's tremendous growth has resulted in a substantial rise in the cost of inspection. Because of these costs, a closer scrutiny of existing inspection methods has become necessary so as to determine if more efficient and less costly ways could be devised. The purpose of this study, therefore, was to explore the possibility of developing a predictive model for the prevalence of disease conditions in broiler chickens during routine post-mortem inspection. Based on such a model, it was hoped that less costly inspection procedures, which would not compromise public health safety, could be developed. With this in mind and with the goal being the isolation of those variables which will be useful predictors of condemnation rates, the need to systematically examine the interrelationships and interactions of all potentially useful predictor variables was necessary. For such a task, systems analysis and multivariate analytic methods were selected. The systems concept is a well tested problem-solving tool widely accepted in engineering, economics, ecology and human medicine. In veterinary medicine, it is relatively new but is now being applied to solving epidemiologic problems.

The application of multivariate techniques to develop predictive or discriminative models is also widely used in various scientific and social disciplines where the background in the use of quantitative methods is well established. It is a standard statistical tool, the basis of which rests on sound mathematics. Although not widely used in veterinary medicine, examples of the applications of such analytic methods are available.

In the area of poultry health, the application of the systems concept and multivariate analytic models appears limited. However, in one recent study, the relationship between various turkey production factors, and

condemnation and downgrading in turkeys were examined by using factor analysis. Using the 1977 live bird production and processing data from one processing plant in California, the study indicated that, week of year placed, climate on day of processing and feed conversion may have predictive value.

Since the application of systems analysis and multivariate models in veterinary medicine and more specifically in poultry health research is rather scanty, it is believed that the results of this study may have broader benefits in examining comparable scientific problems.

The poultry systems approach: The rationale of the study relied on the fact that since it is highly unlikely that diseases suddenly arise in transit (although existing infections could be exacerbated as a result of transit stress) or while birds are under processing, it was rational to think that disease conditions that lead to condemnations during inspection must have had some time to develop and be recognized as lesions. In that case, the infection must have taken place while the flock was still on the farm. This, necessitated a critical examination of the farm ecosystem to isolate and identify variables which would be useful in predicting condemnation rates; this was the task of the research design. Therefore, environmental, managerial, as well as host and agent factors which may affect the incidence of poultry diseases and the condemnation rate at slaughter plants, were scrutinized via causal diagrams and multivariate epidemiologic models designed for possible predictive and/or discriminative purposes. Since poultry (broiler) production involves a sequentially predetermined set of factors which includes breeder flock sources, hatching, brooding, growing and processing, the identifications of potentially useful predictors of the condemnation rate at slaughter were



designed to take the total poultry production ecosystem into consideration.

Procedure for identification of variables: Three subsystems were considered; the hatchery, the broiler house and transit and processing. In the hatchery subsystem, the task was to identify the variables which had potential causal influence on condemnation rates.

The infection in the hatchery may arise via genetic or egg-borne transmission (from breeder flock), or as a result of exposure to infectious agents in the hatchery. The subsequent stages which follow hatching are brooding and growing, which take place within the broiler house subsystem. Again, the birds are exposed to various risk factors in such a setting and epidemiologically relevant factors were identified with the aid of the systems diagram. The last stage in the sequence of poultry production phases were factors related to transit or those that arose while birds were being processed, referred to as the transit and processing subsystem.

Sampling: Five cooperating poultry firms with 5-7 growers per firm were selected to form the study sample. To ensure a representative cross section of farms, the study units were selected from three strata of good, average and poor production performance based on criteria provided by the parent firm. The sampling time frames were longitudinal during which time the health status of the population of cohorts and specified multivariable data which affects the condemnation rate were collected. By definition, a cohort of birds that were sequentially monitored during the three phases of broiler operation (hatchery, broiler farm, and processing plant), were referred to as a brood cycle. It requires about 50 days to raise a bird to the desirable marketing weight as a broiler. The data collection time frame was one complete year during which time data on 5 brood cycles were collected. After an initial data gathering visit to a hatchery where the



study farm chicks were hatched, each study farm was visited at two different time periods; one when a given brood of birds were about four weeks old, and again when they were about six to seven weeks old. The last stage of the sample data collection time frame involved obtaining condemnation records of study flocks the gathering of serum for serological analysis and whole bird samples for gross pathological studies in the laboratory.

Types of data: Preexisting data (e.g. condemnation rate at processing, weekly mortality rate etc.) were collected from records kept by the firm, the farm or from the processing plants. Others were generated from field observations (e.g. management variables, weekly feed utilization rate etc.).

Finally, laboratory data were generated from serological and necropsy profile studies where a predetermined samplesize of 200 randomly selected birds were examined. Sera were tested for three indicator diseases using the HA/HI test. These disease agents were Newcastle, disease virus Mycoplasma gallisepticum and Mycoplasma synoviae. The necropsy task involved gross pathological examination of the birds for any abnormal tissue changes which could be attributed to diseases.

Data processing: Since the raw data collected from the various data generating centers had to be stored, retrieved and analyzed using a computer, a specific file handling software was developed for local use. The software used BASIC language and was designed in an interactive mode. The data were stored on floppy diskettes in a model II Radio Shack microcomputer. At the time of data analysis, the information was transferred to a larger central computing facility. The analysis of the data was performed using BMDP statistical software, on a VAX 11/750

computer at Tuskegee Institute. The specific BMDP statistical programs used were: P2D for descriptive statistics, P6D for examining scatter plots of variables, P1R and P2R for multiple and stepwise regression analysis and P7M for conducting stepwise discriminant analysis to develop a classification function into high or low condemnation groups. The final screening of variables to arrive at the best set of predictor or discriminator variables was accomplished by a computerized stepwise selection process which utilized forward and backward stepping techniques. In this procedure, the criterion for adding or deleting a predictor variable equivalently involved reduction in sum of squares, partial correlation coefficient, or an evaluation of the F statistic. Once a set of predictor variables were identified, the resulting model was examined further by performing residual analysis to evaluate the adequacy of the model. A variety of residual plots were employed to identify the nature of fit, outliers, deviation from normality and other deficiencies.

Predictor model: The data base contained a maximum of 154 cases for 141 variables. These variables formed the initial data matrix upon which the various BMDP statistical programs were run. Since the objective was to develop a predictive model, only the multivariate data analyses are presented. The first step was to reduce the lengthy list of variables via systematic screening to a more manageable level, which was arbitrarily set at about 30-50 predictor variables. The final model for a subset of predictor variables was then selected from these. In such a variable reduction step, one consideration was to delete all variables which were of local significance to the study region so that only variables which were of local significance to the study region could be generalized to other areas were utilized in the analysis. Included in such omissions were the significant variables representing hatchery source, vaccine source and location of air intakes or exhausts.

Via regression analysis, the best predictor model was determined to be:

$$\begin{aligned} \hat{Y}_2 = & 19.3543 - 0.21023X_{63} + 0.10855X_{14} + 0.20511X_{109} \\ & + 0.3227X_{129} - 0.4371X_{205} - 0.00702X_{223} + 0.18366 Y_{2T} \\ (R = 0.91, R^2 = 0.82, F \text{ ratio} = 19.07) \end{aligned} \quad (1)$$

Where:

$Y_2$  = predicted overall condemnation rate (%) due to diseases,

$X_{63}$  = the average hatchability rate (%) for the hatchery,

$X_{14}$  = the total number of genetic strains of birds on the farm,

$X_{109}$  = the disease rate variable (%) derived from necropsy examination of poultry

$X_{129}$  = water spacing per bird in inches

$X_{205}$  = total precipitation (inches) during a brood cycle,

$X_{223}$  = the distance from the poultry farm to the processing plant (miles)

$Y_{2T}$  = the overall condemnation rate due to disease (%) during one previous brood cycle.

This equation was obtained at the end of the forward stepping regression analysis program. The finding was consistent with the underlying biological expectation in regards to the variables with a positive relationship to  $Y_2$ . For example, if the previous condemnation rate ( $Y_{2T}$ ) was high, one may expect the current condemnation rate or the response variable ( $Y_2$ ) to also be high. The positive relationship between  $X_{14}$  and  $Y_2$  says that if the number of genetic strains kept on a poultry farm are large, this leads to high



condemnation rates. This of course could be a reflection of limitations in the management or that the chances of getting poor doers from among a larger genetic pool is greater than that from a few which would have been selected specifically for good performance. A similar management related argument could be made for  $X_{129}$ . The variables with an inverse relationship,  $X_{63}$ ,  $X_{205}$  and  $X_{223}$  are not so straightforward to explain except for the first case. If the hatchability rate ( $X_{63}$ ) is high, this could be indicative of good management and therefore the returns in lower condemnation rates at processing may be expected. The model indicate that the total precipitation during the brood cycle ( $X_{205}$ ) is inversely related to condemnation rate. Although this could be questionable, one reason here may be that significant precipitation is observed during the spring or early summer months which may be the most conducive times for raising poultry. This may be partly due to the cleansing effect that rain may have on infectious agents in the air. The variable for distance from the farm ( $X_{223}$ ) is somewhat peculiar in the sense that one would in fact expect to see a positive influence of  $X_{223}$  on  $Y_2$  i.e. as the distance increases, the birds are exposed to more stress due to travel which may then exasperbate existing abnormalities leading to higher condemnation rates. However, the relationship in the model was inverse. This can only be speculated here in that possibly due to the fact that transit stress is known to be harmful to animals in general, the management may have provided above average care at the time of transporting of birds to the processing plants.

An examination of the standardized regression coefficients given in equation 2 is useful in providing comparative information on the

importance of each predictor variable.

$$Y_2 = -0.48X_{63} + 0.12X_{14} + 0.51X_{109} + 0.11X_{129} - 0.5X_{205} - 0.2X_{223} + 0.15 Y_{2T}$$

$$(R = 0.91, R^2 = 0.82, F \text{ ratio} = 19.07) \quad (2)$$

In this case,  $X_{109}$  was the most valuable predictor followed by  $X_{205}$ ,  $X_{63}$ ,  $X_{223}$ ,  $Y_{2T}$  and finally  $X_{14}$  and  $X_{129}$ . For the predictor equation, the  $R$  and  $R^2$  values were 0.91 and 0.82 respectively. This was a very high correlation coefficient and the equation successfully explained 82% of the variability in  $Y_2$ . It also had a significant  $F$  ratio of 19.07 which showed strong linearity between  $Y_2$  and the independent variables.

An essential part of any regression analysis is a careful examination of residuals to ensure that the assumptions of least squares theory are fulfilled. Therefore, residuals of the predictor model were scrutinized with the aid of computer plots. In the first plot, the objective was to examine the distribution of  $\Sigma i$  about the mean (zero). A plot of  $\Sigma i$  vs the predicted  $\hat{Y}_i$  indicated that the residuals appeared to be randomly distributed around the zero mean in a balanced manner i.e. about half of the cases were positive (above 0), while the rest were negative (below 0). The residuals were all within an acceptable standard deviation of  $\pm 2.0$ . In a second case, the squared value of the residuals  $(\Sigma i)^2$  were plotted vs the predicted  $\hat{Y}_i$ . As expected, this showed a clustering of most of the  $\Sigma i^2$  close to zero. Therefore, there were no major problems with outliers and in terms of model inadequacy.

**Discriminant models:** To perform the analysis for developing the linear discriminant functions to classify a flock into high or low condemnation groups at the time of processing, various

decision-making options were tried. These included criteria for high or low condemnations set at 5%, 2%, 1%, 0.5% and 0.1%. These demarcations were set somewhat arbitrarily but with the idea of providing a variety of options for consideration.

The dependent variable used to develop the discriminant models was the overall condemnation rate due to diseases ( $Y_2$ ). To perform the stepwise discriminant analysis, the F-to-enter and F-to-remove values were set at 4.0 and 3.996 respectively. For the two categories of condemnation rates (high or low), prior probabilities were set at 0.5.

Two cases were selected and presented here for demonstration purposes.

Case 1: Demarcation between high and low condemnation rate set at 1%

$$\begin{aligned} LC = & 4091.15234 + 114.77283X_{60} + 47.4403X_{61} + 44.89433X_{63} \\ & + 44.96988X_{64} - 18.59022X_{14} + 11.94752X_{109} + 48.3914X_{205} \\ & - 4.75752Y_{2T} + 34.62482X_9 \end{aligned} \quad (3)$$

$$\begin{aligned} HC = & -3969.55249 + 107.6714X_{60} + 44.38445X_{61} + 44.18753X_{63} \\ & + 44.3899X_{64} - 17.56498X_{14} + 12.64814X_{109} + 45.09671X_{205} \\ & - 0.93103Y_{2T} + 31.05351X_9 \end{aligned} \quad (4)$$

Percent correct classification overall = 91.9

Percent correct classification for under 1% = 93.1

Percent correct classification for over 1% = 87.5

Case 2: Demarcation set at 0.5%

$$\begin{aligned} LC = & -4863.71973 + 78.50391X_{60} + 77.2642X_{62} + 28.68584X_{64} \\ & - 85.92729X_{129} - 8.73708X_{205} + 1.32762X_{223} \end{aligned} \quad (5)$$

$$\begin{aligned} HC = & -4699.33447 + 76.82549X_{60} + 75.34322X_{62} + 28.30284X_{64} \\ & - 83.62469X_{129} - 7.79638X_{205} + 1.21017X_{223} \end{aligned} \quad (6)$$



Percent correct classification overall = 94.6

Percent correct classification for under 0.5% = 88.2

Percent correct classification for over 0.5% = 100

Where:

LC = equation for low condemnation rate group,

HC = equation for high condemnation rate group,

$X_9$  = strain group

$X_{14}$  = total number of strains on farm

$X_{60}$  = incubator type

$X_{61}$  = incubator type

$X_{62}$  = average fertility rate (%) for hatchery

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{64}$  = average fertility rate (%) for brood of birds

$X_{109}$  = average disease rate (%) based on necropsy at 7 weeks

$X_{129}$  = water spacing per bird in inches

$X_{205}$  = average total precipitation for study brood (inches)

$X_{223}$  = distance from farm to plant (miles)

$Y_{2T}$  = previous condemnation rate (%) due to diseases for study farm

In each of the discriminant models, a classification function to specify whether a flock should be categorized into a high (HC) or low condemnation (LC) group are provided. In each case, a flock was assigned to the group (HC or LC) with the largest value of the classification function. These equations were coupled with the respective correct classification probabilities. The probability of correctly classifying a flock into high condemnation category ranged from 87.5% to 100%. The range for classifying into low condemnation category was 88.2% to 93.1%, with an

overall correct classification probability of 91.9 to 94.6%. This indicates that the accuracy of the model in providing decision-making information was, therefore, reliable.

It should be noted that the objective in this study was to develop a predictor model which could serve as an adjunct to the existing poultry inspection procedures and standards. Therefore, the results presented are visualized in terms of whether a decision pertaining to the current inspection procedure is to be made may involve either a scaled down procedure which in effect means that the processing line speed may increase or to maintain the status quo currently operational in the various processing plants.

In order to effectively utilize the models, two prerequisites should be fulfilled. Firstly, information for the variables identified in the equations should be made available by the firm/farm at the time of processing or immediately prior to processing of the birds. Secondly, the veterinarian, must take the data for the variables selected and generate a value for  $Y_2$  which is the predicted condemnation rate for the particular flock to be processed. Finally, using the values computed, the veterinarian decides on whether to introduce scaled down inspection procedure or maintain the regular inspection routine. Based on current information, the veterinarian could for example use a microcomputer and obtain a set of instructions to facilitate the decisionmaking task for the type of inspection best suited to individual flocks. Such a computer program was prepared using BASIC. The program is interactive with a menu format where one pursues available alternatives and responds to those questions until the objective has been achieved.

Note that, via such microcomputers located in the various poultry processing plants throughout the country, one could maintain a network of information gathering devices with connections to a central data base in some specified place. Since such a data base would be inherently rich and reliable in the case of poultry, one maybe in a position, not only to use microcomputers for implementing the models in the field, but one could also utilize the data base for other problem-solving tasks. Therefore, it is felt that one of the best alternatives for implementing the use of the predictor models in the field could be via the introduction of microcomputer to facilitate data handling and decision-making in poultry inspection. This would be of great benefit to the poultry industry and to the veterinary profession itself, whereby, for example, some of the expertise of veterinarians and poultry inspectors may be diverted to expand the utilization of current information technology in their respective areas.



Personnel: Flock Testing Feasibility Study Project

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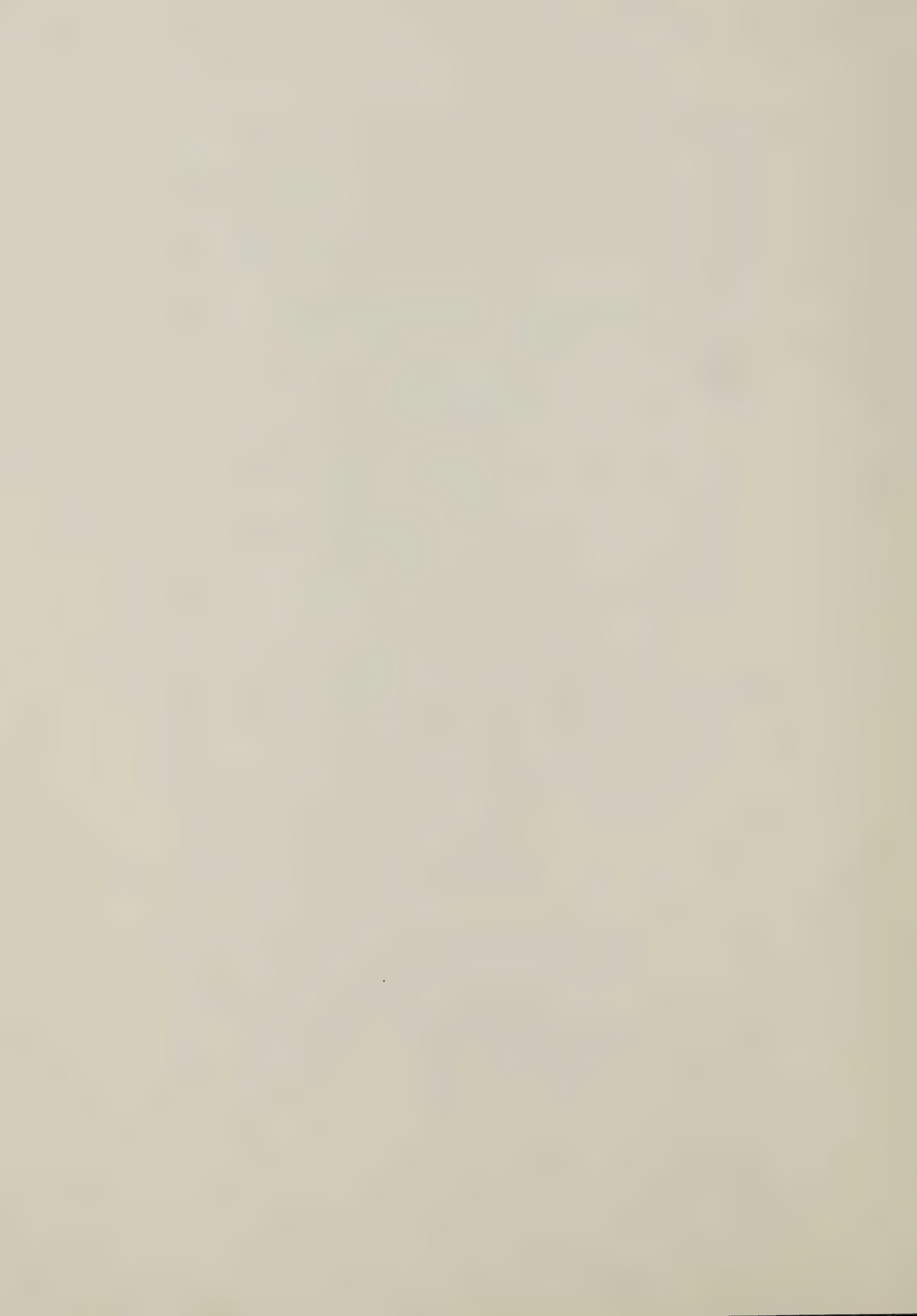


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## 1. INTRODUCTION

The precursor to a problem-solving task such as in the case at hand, involves firstly a definition and a detailed description of the problem under study so that the objectives to be attained could be better focussed. In this case, a brief review of poultry inspection and the problems associated with it as well as a description of the poultry industry, followed by a review of the biodynamics of poultry health provides an adequate background to comprehend and appreciate the complexities involved in this study.

1.1. The Problem: The poultry industry has seen tremendous growth since 1959, when inspection of poultry first became mandatory. The total volume of poultry products slaughtered under Federal inspection rose from 5 billion pounds (lbs) in 1960 to 16.5 billion lbs in 1981. More specifically, there has been an increase in broiler production (1.5 billion broilers slaughtered in 1960 to 4.1 billion in 1981, (1-5). Such increases in production have caused higher inspection costs on one side, while also leading to higher speed processing lines (23 birds per minute, per inspector on the average) to keep up with higher processing rates. This, no doubt, has resulted in increased efficiency of processing plants, but it may have diminished the accuracy and consistency of inspection. Correspondingly, the cost of inspection has steadily risen and when compounded with the inflation rate, a closer scrutiny of existing inspection methods and other research into possible cost reducing

inspection alternatives seemed timely.

The responsibility of poultry inspection falls under the jurisdiction of the Food Safety Inspection Service (FSIS) of the United States Department of Agriculture (USDA). Annually, over 4 billion slaughtered birds to be inspected by FSIS personnel in accordance with the amended Poultry Product Inspection Act (PPIA) of 1968. This program is responsible for assuring poultry and poultry products slated for commerce in the United States (U.S.) are inspected to provide confidence to consumers that such products are wholesome, unadulterated and truthfully labelled. The inspection law covers raw carcass poultry (except for small farm flocks), as well as all processed poultry products such as frozen dinners and soups. About 3000 processing plants which slaughter and/or further process poultry are under inspection by FSIS. Only 245 of these slaughter young chickens. Chickens comprise 96 percent (%) of the slaughter and turkeys, ducks, geese and guinea fowl comprise the remaining 4 percent (16).

The process of inspection, although standard and comparable from plant to plant, requires careful and diligent supervision and execution of tasks by well trained personnel. It consists of ante-mortem (before death) and post-mortem examinations. Ante-mortem inspection for disease involves making spot checks on the health of birds as they arrive at the processing plant so that those which are already dead, or those which appear unfit for slaughter,



are automatically condemned and destroyed. The slaughtered bird carcass and its internal organs are individually examined on high speed processing lines for diseases or conditions which would cause all or part of the carcass unfit for human consumption. To assure uniformity and effectiveness of the inspection process, USDA veterinarians supervise the post-mortem inspection procedures and other duties performed by food inspectors.

In recent years, inflation and increased productivity in the poultry industry have been straining the inspection costs, which is borne by appropriated Federal funds except for inspectors' overtime work. To help control costs and ensure consumer protection, FSIS has been developing and reviewing inspection procedures to determine more efficient ways to inspect poultry and poultry products. For example, most young chickens or fryers are now inspected under the procedure known as a modified traditional inspection which makes use of a mirror to reflect the back side of a bird, thus reducing the need to manually turn over the carcass as in the traditional method. This newly implemented procedure (April 1979) has been shown to save inspection time and the inspectors' task has also become less tiring (6).

Other ways of lowering inspection costs are also being considered, and the one that is the central theme of this report is that of flock testing. This new approach to inspection may offer considerable savings in manpower. This potential could be realized if it is possible to predict the

types and prevalence of disease conditions in poultry flocks before they are slaughtered; and then develop a scaled down inspection procedure which could be safely used to inspect flocks where the predicted incidence of disease is low. The rationale for such an approach is quite simple. Most poultry, especially broilers, are raised and brought to market under highly controlled conditions by an industry which is vertically integrated such that one firm has control of breeding, hatching, feeding, growing and slaughtering. Since the birds' genetic potential and environmental determinants are closely monitored to attain maximal growth with minimal losses due to diseases, the condition of birds in a flock tends to be quite uniform and homogeneous. It may then be possible to determine the health status of such a population of birds by examining the performance records and other possible indicators of health, and by inspecting a representative sample from the flock before slaughtering the entire flock. In light of the decline in condemnation rates due to diseases among poultry, flock testing which relies on population health indicators may prove to be useful and appropriate.

- 1.2. The Objective: It is with this background that the contract to conduct a "Flock Testing Feasibility Study" was awarded to the School of Veterinary Medicine of Tuskegee Institute on September 30, 1980. The specific objective of this contract was to determine whether it is possible to predict, accurately and by practical means, the presence and

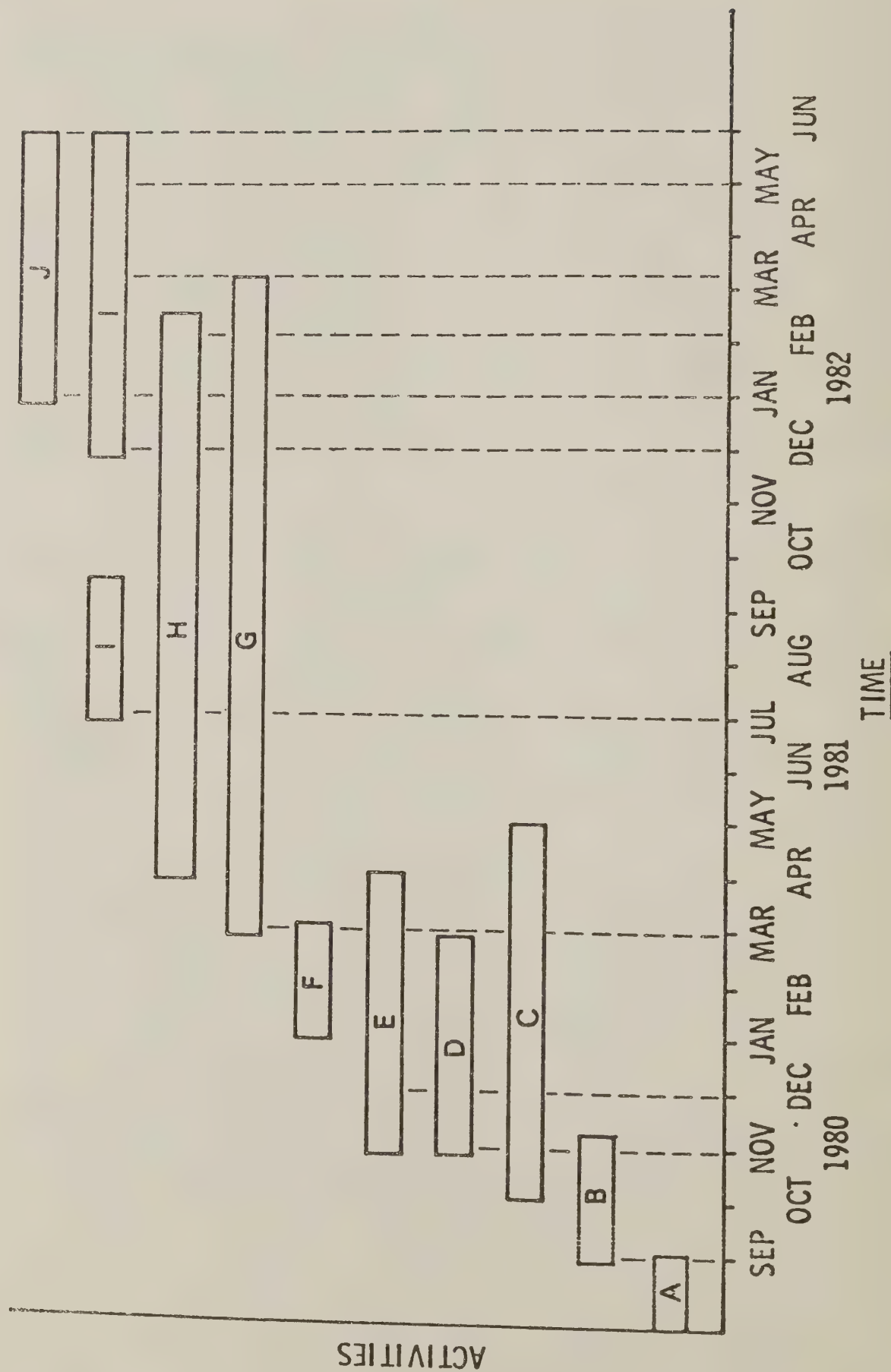
incidence of those conditions in broiler chickens observed during routine post-mortem inspection and which may be a cause for condemnation of all or part of the carcass.

The purpose of the research design was directed at exploring the possibility of developing a predictive model to determine prevalence of disease conditions in broiler chickens during routine post-mortem inspection. Based on such a model, it is hoped that less costly inspection procedures, which would not compromise public health safety could be developed.

The contractual agreement for this project was signed on September 30, 1980, and the date of approval by the Office of Grants Management of Tuskegee Institute to proceed with the project was made on November 1, 1980. The actual implementation of the project officially began on February 15, 1981, with its termination date slated for June 30, 1982. Initially, activities and estimated times for completion of the tasks were outlined in a graphical procedure for analytical and synthetical evaluation and program review (GASP) chart. A modified version of that chart is indicated in figure 1. Since the study was centered around the poultry industry in Alabama, a brief review of the study area appears pertinent at this time.



Figure 1 GASP CHART - SCHEDULE ACTIVITIES AND ESTIMATED TIME  
FOR THE FLOCK TESTING FEASIBILITY STUDY  
School of Veterinary Medicine, Tuskegee Institute (1981/82)



KEY FOR GASP CHART

## TASK - FLOCK TESTING FEASIBILITY STUDY

REFERENCE	ACTIVITIES DESCRIPTION	ESTIMATED COMPLETION DATE
A	Proposal preparation	September, 1980
B	Finalize contract	November, 1980
C	-Develop an Epidemiologic format for flock testing study	May, 1981
	-Initiate contact of farms and processing plants	
	-Prepare data collection and coding format	
D	Finalize arrangements with farms and plants	March, 1981
E	-Hire personnel	April, 1981
	-Purchase equipment/supplies	
F	Conduct pilot studies	March, 1981
G	Data collection	March, 1982
H	-Develop file handling software	February, 1982
	-Code data and enter on computer	
I	Data analysis and interpretation	June, 1982
J	Prepare final report	June, 1982
K	Begin Phase II of study	Undetermined

## 2. THE POULTRY INDUSTRY IN ALABAMA

2.1. Background of Industry: In broiler poultry production, Alabama is ranked third in the U.S. preceded by Arkansas and Georgia (Table 2). The poultry industry in the state is sizeable and diverse in nature, ranging from small independently operated farms to large integrated firms with 10,000 chickens or more per grower. There are 11 major integrated broiler companies in Alabama (7). The number of growers per integrated firm is variable as is the size of the poultry population per grower. Most of these growers are located in the northern and southeastern parts of the state. (Figure 2).

In 1980 and 1981, 39,309,000 and 42,149,000 birds respectively were inspected by FSIS personnels in Alabama. During this period, the condemnation rate in the state varied from 1.32% to 2.19% on a monthly basis; the national figure for condemnation varied from 1.57% to 2.25% for the same period. The average annual condemnation rate for Alabama in 1979 and 1980 was 1.93% and 1.72% respectively. The figure for the same period for the U.S. was 2.01% and 1.84% respectively, indicating that the rate was declining (Table 2) in the state as well in the country as a whole. The disease specific condemnation rates for the five major poultry producing states for the period 1976-1982 is given in Table 3. The values for 1982 are incomplete.

In Alabama, as well as in other states, the vertically integrated firms operate their own breeder flocks, hatching,



Table 2.

COMPARISON OF YOUNG CHICKENS SLAUGHTERED UNDER FEDERAL INSPECTION IN  
THE TOP FIVE (5) BROILER PRODUCING STATES (1975-1982)

(Number of Chickens In 1000's)

		ARKANSAS	GEORGIA	ALABAMA	N.C.	MISSISSIPPI
1982	No. Inspected	49,857	43,711	37,261	33,479	21,060
	Post. Cond. (%)	1.66	1.83	1.55	1.82	1.79
1981	No. Inspected	51,618	49,109	42,149	34,903	23,817
	Post. Cond. (%)	1.82	1.66	1.57	1.58	1.70
1980	No. Inspected	49,011	45,952	39,309	33,483	23,124
	Post. Cond. (%)	1.95	1.68	1.72	1.66	1.83
1979	No. Inspected	48,845	42,301	36,499	29,193	21,581
	Post. Cond. (%)	2.20	1.78	1.93	1.72	2.01
1978	No. Inspected	46,075	42,440	35,208	27,928	21,940
	Post. Cond. (%)	2.09	1.89	1.78	1.83	1.84
1977	No. Inspected	39,586	36,076	30,533	26,461	19,436
	Post. Cond. (%)	2.42	1.86	2.69	2.11	1.55
1976	No. Inspected	41,531	37,575	33,734	25,629	21,768
	Post. Cond. (%)	2.07	1.51	2.08	1.69	1.58
1975	No. Inspected	36,838	34,250	31,938	22,588	19,327
	Post. Cond. (%)	1.95	1.37	1.70	2.14	1.66

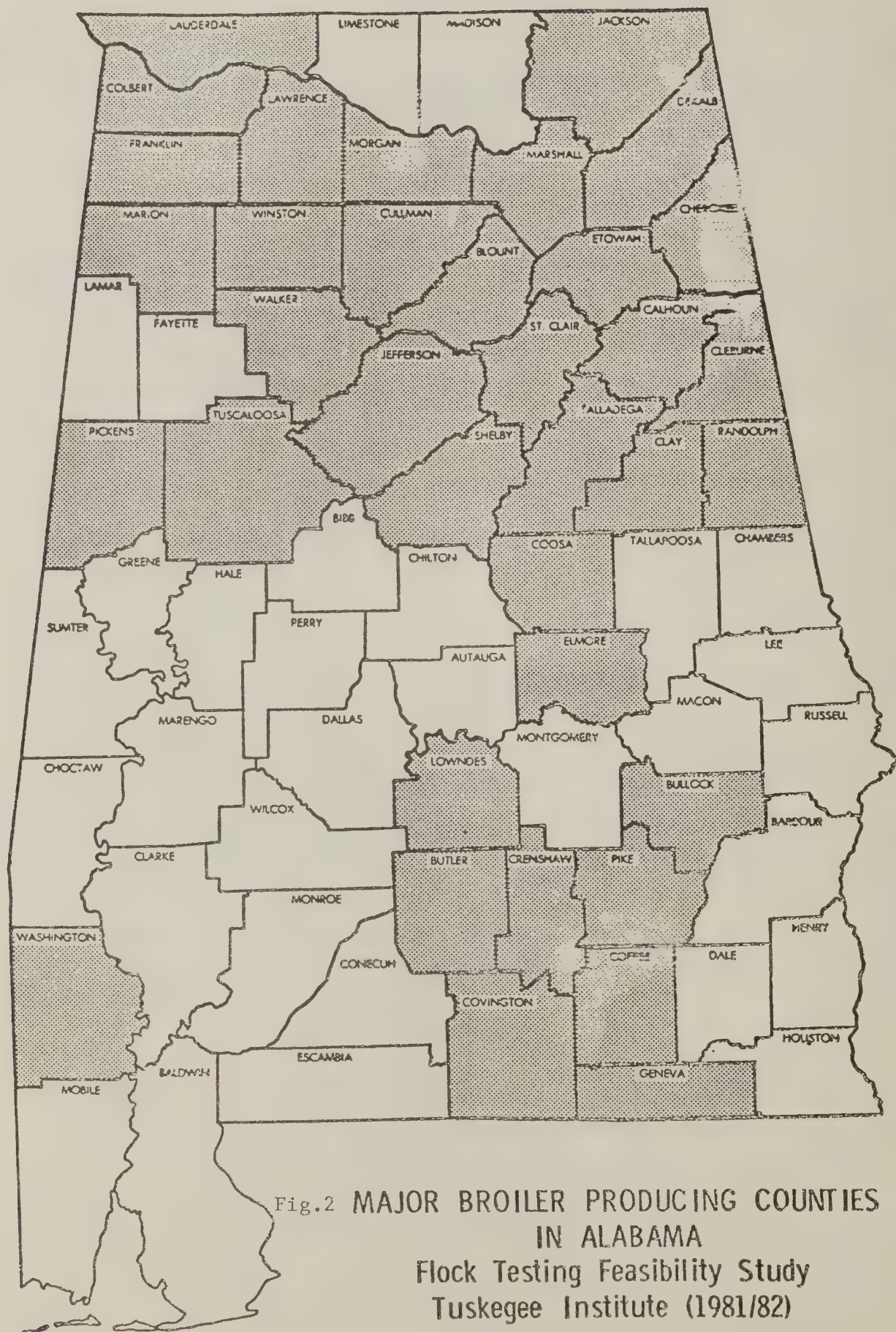


TABLE 3 YOUNG CHICKENS CONDEMNATION RATES IN THE TOP FIVE  
POULTRY PRODUCING STATES DURING 1975 - 1982

STATES		DISEASE SPECIFIC CONDEMNATION RATE (%)							
		LEUCOSIS	SEPTICEMIA	AIRSACCULITIS	SYNOVITIS	TUMORS	OTHERS		
Arkansas	1982	0.02	0.46	0.35	0.02	0.04	0.02		
	1981	0.03	0.44	0.35	0.02	0.03	0.03		
	1980	0.08	0.47	0.37	0.02	0.03	0.03		
	1979	0.09	0.49	0.41	0.02	0.02	0.05		
	1978	0.05	0.40	0.24	0.02	0.02	0.07		
Georgia	1977	0.37	0.43	0.28	0.02	0.01	0.05		
	1976	0.21	0.26	0.26	0.01	0.01	0.07		
	1975	0.15	0.24	0.22	0.02	0.01	0.10		
	1982	0.05	0.43	0.39	0.004	0.04	0.03		
	1981	0.02	0.41	0.28	0.01	0.03	0.04		
	1980	0.02	0.48	0.29	0.01	0.02	0.03		
	1979	0.05	0.47	0.28	0.01	0.08	0.03		
	1978	0.02	0.36	0.34	0.01	0.02	0.08		
	1977	0.13	0.30	0.34	0.01	0.01	0.11		
	1976	0.07	0.20	0.13	0.01	0.01	0.14		
Alabama	1975	0.12	0.19	0.09	0.01	0.01	0.02		
	1982	0.04	0.38	0.24	0.01	0.01	0.03		
	1981	0.35	0.26	0.01	0.04	0.03	0.04		
	1980	0.09	0.39	0.26	0.01	0.02	0.04		
	1979	0.11	0.43	0.35	0.01	0.02	0.07		
	1978	0.05	0.30	0.20	0.02	0.02	0.09		
	1977	0.19	0.47	0.67	0.02	0.02	0.12		
	1976	0.09	0.36	0.23	0.02	0.01	0.12		



TABLE 3 YOUNG CHICKENS CONDEMNATION RATES IN THE TOP FIVE  
POULTRY PRODUCING STATES DURING 1975 - 1982

STATES	DISEASE SPECIFIC CONDEMNATION RATE (%)							
	LEUCOSIS	SEPTICEMIA	AIRSACCUITIS	SYNOVITIS	TUMORS	OTHERS		
1975	0.08	0.33	0.19	0.02	0.01	0.12		
North Carolina								
1982	0.05	0.64	0.44	0.004	0.04	0.04		
1981	0.03	0.52	0.29	0.01	0.04	0.04		
1980	0.04	0.53	0.28	0.003	0.03	0.06		
1979	0.05	0.48	0.29	0.004	0.03	0.06		
1978	0.07	0.42	0.30	0.01	0.02	0.05		
1977	0.16	0.35	0.19	0.01	0.02	0.10		
1976	0.15	0.27	0.17	0.01	0.01	0.13		
1975	0.19	0.24	0.16	0.01	0.01	0.12		
Mississippi								
1982	0.11	0.41	0.45	0.01	0.02	0.02		
1981	0.05	0.04	0.31	0.01	0.01	0.01		
1980	0.09	0.41	0.27	0.01	0.01	0.02		
1979	0.12	0.46	0.24	0.01	0.01	0.03		
1978	0.07	0.35	0.23	0.02	0.01	0.03		
1977	0.16	0.30	0.18	0.01	0.02	0.02		
1976	0.19	0.21	0.12	0.02	0.01	0.07		
1975	0.19	0.16	0.17	0.02	0.01	0.12		



growing, feeding and slaughtering. These operations are closely supervised. However, there are managerial variabilities amongst firms. Each firm has growers which could be categorized as above average, average and below average based on performance characteristics which are further defined under methodology for stratified sampling. The major poultry firms in the state are either national or independents companies. Such a combination of independent and national firms provide the state with a representative blend of the poultry industry in the U.S.

2.2. Typical Poultry Production Process: A typical broiler raising enterprise consists of a source of breeder flocks which provide the high quality eggs for hatching. The genetic make up of breeder flocks in Alabama are mainly of the Corbett, Arbor Acres, and Peterson strains. The eggs from such breeder flocks are taken to hatcheries where under optimally controlled temperature and relative humidity conditions, the eggs are set and hatched after a period of 21 days. An important factor in the management of the hatcheries is the control of incubator temperature and sanitation of the environment in the hatchery. Hatching egg quality, fertility, hatchability and chick quality are an interrelated set of events that ultimately affect the cost of production. So, the sanitary management of the hatchery becomes crucial.

Sanitation in a hatchery typically involves washing, fumigating and disinfecting. The disinfectants utilized are

quaternary ammonium compounds, organic iodine combinations and phenol. In the application of these chemical agents, manufacturer's recommendations are followed.

The cleaning and disinfecting procedures vary somewhat depending on the parts of hatchery as described below:

- Setters- in some hatcheries, the setters are sprayed three times per week with a solution of quaternary ammonia. In addition, broken eggs and debris are removed from the bottom portion of the setter on a weekly basis. Every four months, the setters are scrubbed with a commercial detergent and rinsed with hot water using a high pressure sprayer, followed by a disinfectant such as quaternary ammonia compound. In others, the setters are washed every six months with a commercial detergent and rinsed with cold water under high pressure.
- Hatcher- after the chicks are removed, the hatcher is rinsed with water and drained. Scrubbing with a detergent solution and rinsing with hot water under high pressure ensues. This is followed by the application of a disinfectant solution such as a quaternary ammonia compound or iodine solution.
- Vaccinating machines- are hand cleaned daily with a detergent solution. Rinsing with cold water follows. Needles are autoclaved every day and changed twice a day.
- Floors and hallways- are washed with hot water under

high pressure and sprayed with a disinfectant such as a quaternary ammonia compound every hatch day. In some hatcheries, the work rooms are fumigated three times per week with a quaternary ammonia solution.

- Chick buses- are washed with hot water under high pressure two times per week in some hatcheries and once a week in others. A solution containing quaternary ammonia is sprayed on the inside of the buses.
- Hatching crates and egg flats- are washed with hot water and disinfectant on a tray washing machine at the end of every hatch.
- Chick delivery crates- are washed with a disinfectant and hot water twice a week on a crate washing machine.

The above brief glimpse of sanitation practices in a hatchery is one of many managerial responsibilities. After hatching, baby chicks are kept in the hatcher for about 24 hours. During this time, the chicks are not fed. In many of the hatcheries studied, chicks were vaccinated for Newcastle, infectious bronchitis and Marek's disease before they were moved to the broiler houses. The baby chicks were then transported, via chick buses, to the broiler house. In other hatcheries, the chicks were vaccinated within 10-14 days of hatching. Again, good sanitation practices and a warm and comfortable environment during the transition period is important. The chicks are either placed in

partial or whole house brooding. Partial house brooding is an attempt to save cost (energy/heat, space) and maintain the chicks in a smaller confined space, where more birds can huddle, to keep warm, under a few brooders.

The responsibility of brooding and growing birds to marketable weight, at about 50 days of age, rests on each grower. The birds are monitored for feeding, water consumption, disease problems and variations in microclimate within the house. Growers usually cull a proportion of their undersized birds during the first few weeks. Through this practice, the cost of feed can be reduced since the undersized and inefficient birds are depopulated. During the growout period, good farm management practices coupled with a planned disease control program, proper feeding and sanitation, are crucial factors that determine the health status of the population. At the end of the 50 day growing period, a catching crew is brought in and the birds are loaded onto trucks and transported to the respective company slaughter plants. The grower then has about 7-10 days during which time the litter may be changed and the houses cleaned and disinfected in preparation for the subsequent growout or brood cycle.

- 2.3. Processing plants in Alabama: The processing plants in Alabama appear to be representative of the FSIS supervised plants in other parts of the country. There were 25 processing plants operating in Alabama in 1981-82 (8). Some of the plants operate a two shift system, doubling up on



night and day processing. A majority of the plants operate on a regular eight hours a day basis. In terms of inspection, both the traditional and modified traditional procedures are utilized. In the former case, an individual inspector examines both the external aspects of a bird and its internal organs, to determine if it is fit for food. In the newer approach, a team of three inspectors are placed on each line with responsibilities split into an "outside" and "inside-viscera" inspection of each bird. Inspection of the external parts of the birds is facilitated with the aid of a mirror so that the outside "parts" inspector does not have to handle the bird; a mirror behind the carcass makes all surfaces visible. Two inspectors handle the "inside-viscera" or internal organs of the birds. The "inside-viscera" examination has been redesigned so that fewer hand motions are used to check the inside of the carcass and time can be saved, making the process less tiresome. Upon completion of inspection, the birds are chilled and packaged for distribution to consumer outlets.

- 2.4. Is Alabama Representative of the Poultry Industry in the South and in the United States? Among the eleven (11) major integrated broiler companies in Alabama, five are national companies that also have broiler operations in other states; the other six are independent companies owned by individuals or families in the state (Table 4). Among the five firms which cooperated in this study, three were national and the other two were independent companies. Their poultry flocks

Table 4

Broiler Processing Plants and major companies operating in Alabama  
(1981-1982)

Name of Firm	Location	
	City	County
Cagle's Incorporated	Collinsville	DeKalb
Colonial Poultry Co.	Albertville	Marshall
ConAgra Poultry Co.	Athens	Limestone
" " "	Decatur (office)	
" " "	Enterprise	Coffee
Gold Kist Poultry Co.	Cullman (office)	Cullman
" " " "	Boaz	Marshall
" " " "	Guntersville	Marshall
" " " "	Trussville	Jefferson
Golden-Rod Broilers	Cullman	Cullman
" " "	Greensboro	Hale
Marshall Durbin Co., Inc.	Hayleville	Jefferson
" " " "	Jasper	Walker
Peco Foods, Inc.	Gordo (office)	Tuscaloosa
" " "	Tuscaloosa	Tuscaloosa
Poultry Products Co., Inc.	Montgomery	Montgomery
Southland Broilers, Inc.	Enterprise	Coffee
Spring Valley Foods, Inc.	Oxford (office)	Etowah
" " " "	Blountsville	Blount
" " " "	Heflin	Cleburne
" " " "	Gadsden	Etowah
" " " "	Ashland	Clay
Wayne Poultry	Union Springs	Bullock
" "	Decatur	Morgan
" "	Albertville	Marshall

SOURCE: Food Safety and Quality Service, Poultry and Dairy Quality Division, List of Plants Operating Under USDA Poultry and Egg Grading and Egg Products Inspection Program (Washington, D.C., United States Department of Agriculture, 1979), p. 5.

were located in the major broiler producing areas of the state.

Based on the brief presentation given above, Alabama appears to represent the diversity and complexity of the poultry industry in the U.S. The state is in an area where more than 60% of the nation's broilers are produced (Arkansas, Georgia, Alabama, North Carolina and Mississippi). Thus, it was logical to conduct this study in Alabama where the poultry industry is well established and occupies a significant economic position in the hierarchy of agricultural industries both in the state as well as in the entire U.S.

### 3. THE BIODYNAMICS OF POULTRY HEALTH - A SYSTEMS VIEW

3.1. Poultry Population Health Dynamics: Poultry health is a function of a complex set of events and interactions between the host (poultry), disease causing agents and environmental factors. In today's poultry industry, although the presence or level of many of the infectious agents have been reduced and birds are kept in relatively controlled environments, differences in managerial expertise and diligence, as well as variabilities in environmental factors, still remain significant. Such variabilities eventually lead to differences in prevalence of diseases amongst farms and subsequent differences in condemnation rates at the time of processing. In order to reduce the cost of production in terms of factors which have influence on poultry health, a detailed review of the literature and an understanding of biomedical processes as these relate to poultry health is necessary.

As presented earlier, since one deals with relatively uniform flocks on a given farm and the major variability is from farm to farm, such a review of the literature emphasizes population health status indicators of individual flocks of broiler chickens. To be consistent and systematic in such a review, one should preferably start from the breeder flock source and proceed through hatching, brooding/growing and finally, inspection of bird carcasses. In light of this premise and to correlate the subsequent identification and specification of variables which were



used as health status indicators in this study, a sequenced review consisting of strain of birds, hatchery management, brooding, housing, sanitation, vaccination, medications, feed utilization, morbidity and mortality, climate and inspection procedures will be examined; as these may affect ultimate condemnation rates due to diseases. Along with a literature review of the biodynamics of poultry health, and since we utilize a systems approach and multivariate analytic models to analyze the data, a brief review of the literature on the application of such techniques in veterinary medicine may be informative and subsequently follows.

### 3.2. The multiple determinants of poultry health:

- Strains of birds- total performance and resistance or susceptibility to disease varies amongst strains or breeds of birds. Some are resistant to one disease but not to another. For example, several lines of chickens with genetic resistance to Marek's disease have been selected and maintained in the laboratory (9). Thus, knowing which strain of birds is more susceptible to a specific disease that may result in high condemnation, could be helpful in formulating a method to predict condemnation. There are many varieties of poultry, but the more popular meat production male lines are: Hubbard, Cobb, Peterson and Indian River. The popular female lines are: Hubbard, Arbor Acres, Cobb, Indian River, Pilch and

Shaver. Therefore, the genetic potential of a strain of birds, or the performance of the breeder flock as measured by such indices as genetic quality, fertility and hatchability of hatching eggs and chick quality are very critical in determining the health status of a flock of birds.

- Hatchery management- due to a less competent immune system newly hatched baby chicks are extremely susceptible to various diseases. Thus, hatchery sanitation and management are critical in poultry health. Because of the continuous hatching program in the poultry industry, the air in the hatchery may be contaminated with various organisms, although most of these are non-pathogenic, a few pathogenic species can cause serious health problems for the broilers. This is particularly true for some respiratory diseases. For instance, the time between hatching and transporting of chicks out of the hatchery may not seem important, but in reality it is critical. The longer these birds stay in a hatchery, the higher the possibility of their exposure to pathogens such as Aspergillus species. Since the birds do not receive water and feed in the hatcher, to hold the birds in the hatchery for an extended period of time will cause dehydration. Low temperatures or drafts in the hatchery can also add stress to these birds. Those stressed usually have more violent reactions to

vaccinations and are more susceptible to disease agents at the onset or in their later life. In the case of Aspergillus spp., a few spores inhaled by the baby chicks, while they are extremely susceptible, will most likely result in high condemnation at processing because of airsacculitis (9, 10).

- Brooding- in order to reduce the high cost of heating, many poultry farmers resort to partial house brooding instead of the traditional method of whole-house brooding. Some farmers prefer to block off a large segment of the poultry house and use the brooders in a small restricted area. In doing so, large numbers of baby chicks are crowded together, thus, increasing the density of the population (10). Other farmers prefer to turn on every other brooder in the poultry house; though the birds have the same amount of space, they are usually crowded together under the brooder. This in turn also increases the density of the population. Therefore, the type of brooding (whole-house or partial house) may prove to be a potential indicator in predicting condemnation, since crowded conditions created by partial-house brooding may result in higher mortality, increased feed cost and respiratory disease conditions that lead to higher condemnation rates.
- Housing and ventilation- in recent years, houses equipped with 3 or 5 cubic feet per minute (CFM) fans

have become fairly popular in this part of the country and it is anticipated that many more will be built in the near future. Because these houses are closed, with continuous rapid air movement, once a disease agent is present in a house, it will likely spread rapidly. It is thought that birds reared in this type of house may have higher respiratory infection rates than those reared in conventional poultry houses. Thus, comparing condemnation records of flocks reared in conventional houses to those reared in the mechanically ventilated houses with a similar method of management, may prove to be useful in predicting condemnations in the processing plant. Although not correlated with condemnations due to diseases, housing environments and seasons have been shown to lead to increased down-grading of broilers (12, 13, 14). Another vital aspect is that of the density of birds per given area which may affect the performance of broilers. Studies have shown that there is greater bacterial build up when birds are housed at a density of  $0.42\text{m}^3$  as compared to  $0.84\text{m}^3/\text{bird}$  (15, 16, 17). Therefore, densities of bird population could be a useful indicator of population health.

- Feed consumption and feed conversion- a steady increase in feed consumption in young broilers is an indication of a healthy flock. A sudden change in



feed consumption may indicate disease problems or environmental changes. Thus, monitoring feed consumption of broilers throughout the growing period is a potentially useful indicator for predicting the condemnation rate of the flock. Other factors such as mold contaminated feed and their adverse effects on the performance of birds, are of particular concern since moldy corn and other concentrates, including ground feeds often carry mycotoxins. The effect of mycotoxins have been documented previously (18-23). Therefore, the type and source of feed, and its utilization could be useful indicators. Poultry are among the most efficient food producing animals. Flocks with an excellent health status usually attain feed conversion rates of two pounds of feed to one pound of meat. However, during stress and disease conditions, feed conversions usually are much poorer. Since feed efficiency is directly related to the health status of flocks, its correlation with condemnation rates may be crucial.

- Morbidity and Mortality- although these may not necessarily reflect the rate of condemnation, the type and severity of the disease and the time between occurrence of disease condition and processing, may be useful indicators of population health. In some cases, a flock of broilers may be affected with coccidiosis at an early age, and exhibit morbidity

and some mortality, but such an infection usually does not affect condemnation rate. On the other hand, morbidity and mortality caused by airsacculitis, Marek's disease, synovitis and Newcastle disease and infectious bronchitis particularly at 5-6 weeks of age, could lead to an increased condemnation rate. The relationship between mortality and other conditions causing economic losses and types of housing have been studied previously. The results indicated that an automatic curtain house had the least mortality rate and gave the best returns to land, labor and management (24). Therefore, utilizing morbidity and mortality records in conjunction with necropsy records and other data, may serve as a reliable indicator of population health.

- Vaccination- all commercial poultry firms have their own vaccination programs for broilers, some of which are more effective in disease prevention than others. Variations in vaccination programs could make a difference in condemnation. The vaccines commonly employed are for the prevention of Newcastle disease, infectious bronchitis, infectious laryngotracheitis, fowl pox, Marek's disease, infectious bursal disease, etc. The age of birds at vaccination, use of one or multiple vaccines concurrently, use of booster vaccinations, or vaccines made by different

companies, may have important effects on the health and eventually affecting condemnation rate of the flock (25-31). Therefore, the history of vaccinations may prove to be a useful indicator.

- Medications- most commercial poultry firms institute their own health programs, to provide immediate treatment, when disease conditions are diagnosed. For example, there is definitely a difference in condemnation due to airsacculitis between birds treated with medication and those that were not treated during a mycoplasma infection. A prophylactic medication program specifically aimed at coccidiosis is routinely administered to broilers in the U.S. (11, 31). Use of various coccidiostats and other prophylactic and/or therapeutic medications could be useful indicators of flock health.

- Weather and seasonal differences- most commercial poultry houses are well equipped with heating units, so that the temperature inside poultry houses remains constant during winter months. During summer months, temperatures in chicken houses may increase to 110°F or even higher, particularly in the Southeast and Southwest. In the Fall and Spring, day and night time temperatures fluctuate drastically, (difference of 30-40°F) as a result of these changes birds are under stress and respiratory problems may become serious. Temperature and humidity are important

factors which affect hatchability and chick quality (11), and could eventually reflect in increased condemnations. In order to study the weather and seasonal effect on condemnation, flock performance data collected during different months of the year could be useful.

- Inspection procedures and condemnations - the need to reexamine current poultry inspection procedures with the goal of seeking more efficient and less costly alternatives has recently been addressed (33-40).

Currently condemnations of whole birds in FSIS inspected poultry slaughter plants are grouped by cause into eleven categories viz. Tuberculosis, leukosis, septicemia-toxemia, airsacculitis, synovitis, tumors, bruises, cadavers, contamination, overscald and others. The first six of these are disease categories and amongst these conditions, incidence of condemnation due to septicemia-toxemia has been the highest in the past few years. For example, in 1978, a total of 38,799,191 young chickens were condemned for various reasons and of this total, 13,589,943 or 35% were condemned for septicemia-toxemia, and in 1979, about 41% of the condemnations were due to the same category (41). The increase in numbers of birds condemned for septicemia-toxemia is a significant point and may very well mean that this category of production loss



needs further study (42).

- Sanitation- is the mark of good management and is an area that requires close scrutiny. The economics of today's poultry production mandates high bird densities in commercial operations, which have led to other problems. High bird densities increase the probability of disease spreading via contact and airborne organisms from contaminated dust and air.

These basically are sanitation problems.

It was reported that coliforms represented about 10% of the microbial population of poultry litter (43). Reports also indicate that the housing of birds at  $0.42\text{m}^3$ , as compared to the density of  $0.84\text{m}^3/\text{bird}$ , led to significantly greater bacterial build-up of both aerobic and anaerobic bacteria (15), while dust was shown to be responsible for establishment of the microflora in fresh litter in poultry houses (44). Toxigenic molds, such as Asperigillus, Penicillium, Petriella and Scopulariopsis, have also been isolated from poultry litter (18).

The concern for sanitation in poultry production and processing is two sided. Firstly, to prevent the spread of infections in poultry establishments, and ultimately to protect humans against such organisms as Salmonella, Staphylococcus and Clostridium botulinum (45). Since the air and dust, birds, insects and rodents, equipments and personnel could serve as sources for microbial flora, proper sanitation (washing, disinfecting, etc.) and close

supervision of personnel are crucial in determining poultry health.

With respect to sanitation, one very useful method of surveillance in use in hatcheries and broiler houses is air exposure samplings of these sites to monitor the population size and types of organisms found in the environment. Its usefulness has been documented. In one study, using a New Brunswick STA 200 microbiological air sampler in poultry houses, Bacillus, Micrococcus, Proteus, Pseudomonas, Staphylococcus, four species of Clostridia and nine genera of molds were identified. The author emphasized the need for vigorous sanitation practices, especially in houses with high bird densities, since the numbers of airborne microorganisms in such houses were high (46). The inter-relationship between dust and bacterial contamination and type of houses as well as the air contamination in hatcheries being associated with early chick mortality has been documented (47, 48).

### 3.3. Interrelationships and Interactions Between Factors

Affecting Poultry Health: Although the major determinants of poultry health have been presented briefly, the list of the multiple variables for consideration is rather extensive as will be shown later. The essential point is to recognize that each of these variables are interrelated biologically to directly or indirectly affect poultry condemnations in processing plants. With this in mind and with the goal being the isolation of those variables which will be useful

predictors of condemnation rates, the need to systematically examine the inter-relationships and interactions of all potentially useful predictor variables, using the systems approach, was an obvious and logical choice.

#### 4. FLOCK TESTING - IS IT A RATIONAL ADJUNCT TO POULTRY INSPECTION?

In closing this section on the background preparation required to grasp the problem solving task specified in the objectives of this contract, it is important to interrelate the literature review presented so far, to the overall goal of predicting condemnation rates.

4.1. The Assumptions: It is vital to briefly touch on the idea of why flock testing is a rational adjunct (conceptually to poultry inspection by referring to figure 3 . The diagram presents a summarized list of factors which could affect condemnation rates in processing plants. Some of these factors are related to processing errors e.g. scalding, contamination, improper processing such as bruising, missing viscera, etc. Other factors are related to possible errors during inspection and record keeping, which are present in any human task e.g. experience, fatigue, rapid line speed, etc.

One major assumption is that due to the uniformity of basic training for all FSIS inspectors, the errors that are human related would be comparable among processing plants so that if sample data are collected from various plants, this should not introduce major problems. If so, other than

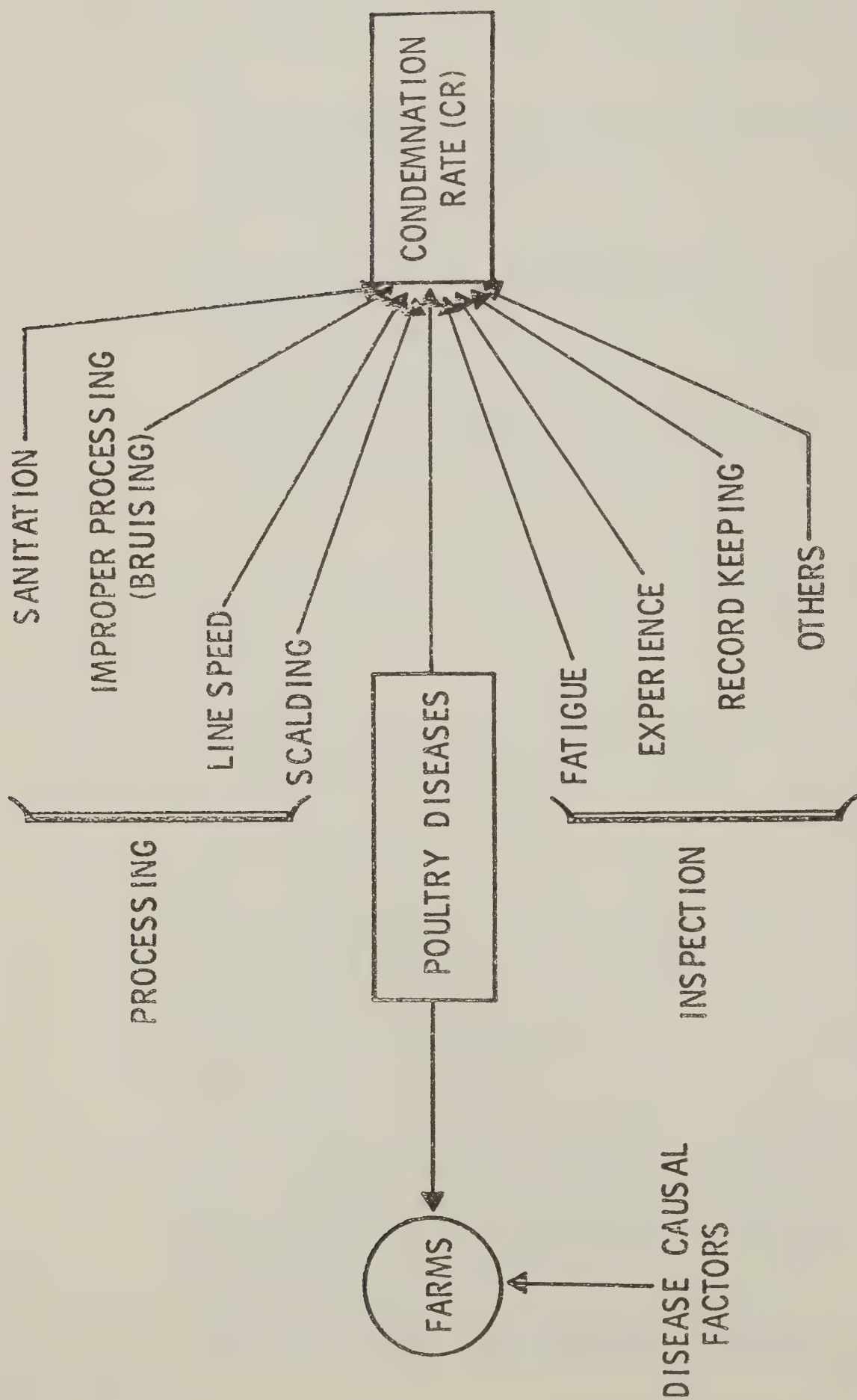


Fig. 3 FACTORS WHICH AFFECT CONDEMNATION RATE (CR) OF POULTRY



processing plant errors, the major determinant of condemnations is disease (figure 3).

- 4.2. The Rationale: Since it is highly unlikely that diseases suddenly arise in transit (although existing infections could be exacerbated as a result of transit stress) or while birds are being processed, it is only logical to think that disease conditions that lead to condemnations during inspection must have had some time to develop and be recognized as lesions, and in that case, the infection must have taken place while the flock was still on the farm. This, of course, necessitated a critical examination of the farm ecosystem to isolate and identify variables which would be useful in predicting condemnation rates; this was the task of this research design.

The above reasoning was supported in another preliminary diagrammatic model (figure 4). For a bird to be condemned due to diseases, in general, the following must hold:

- a. The bird was already diseased (D) on farm or at time of shipping, let us call this:  $P(D)$  = prevalence rate or proportion infected on farm,
- b. The bird is showing lesions (L) for the disease.  
 $P(L/D)$  = probability of finding lesions given that the bird is diseased.
- c. The inspector (I) picks out the lesion correctly.  
 $P(I/L)$  = probability that the inspector correctly picks out the diseased bird, given that the bird

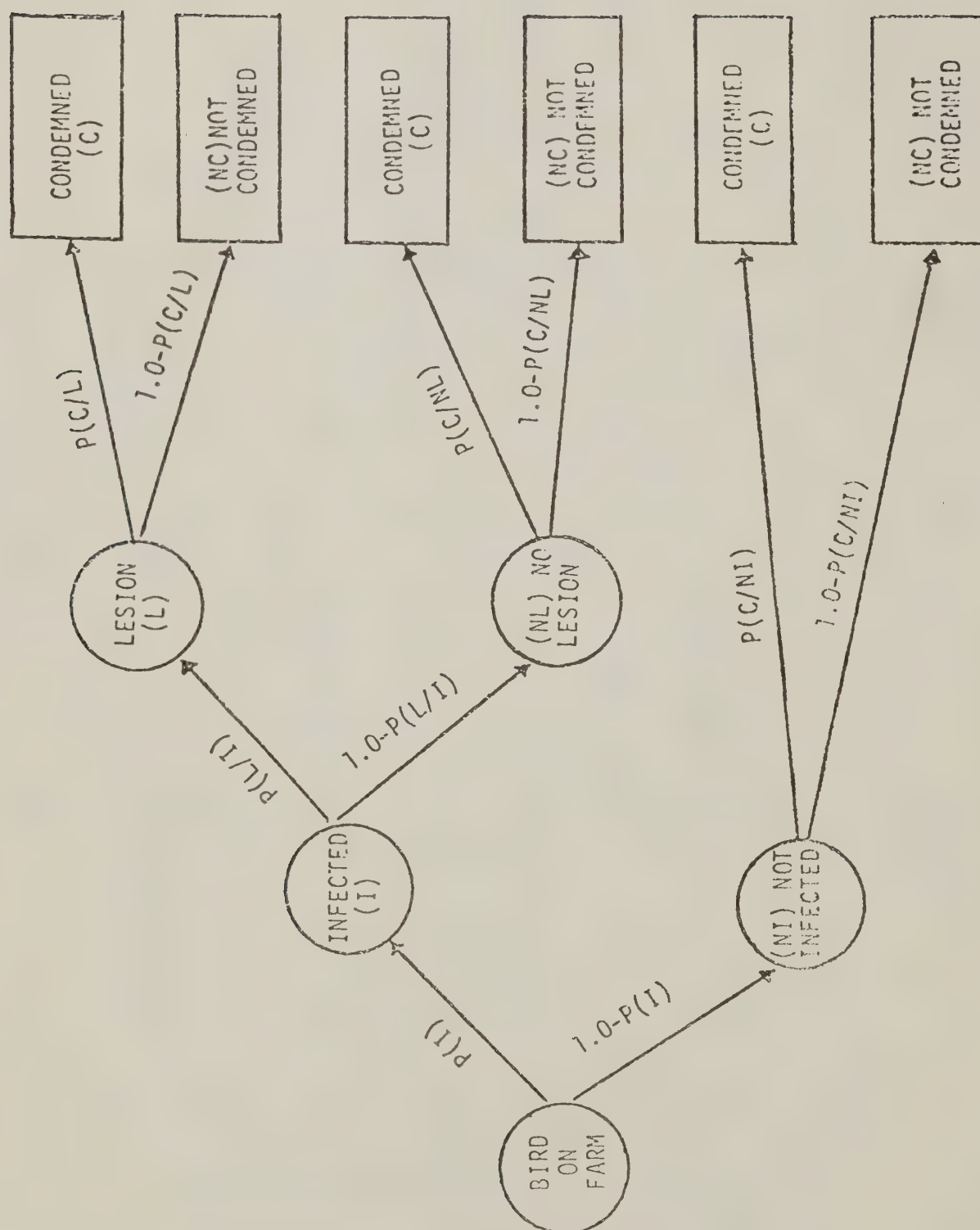


Fig. 4 TREE DIAGRAM FOR A PROBABILISTIC MODEL OF CONDEMNATION RATE OF POULTRY

exhibits lesions.

The figure and the above listed criteria showed that the probability of condemnation was mainly a function of whether a bird was diseased  $P(D)$ , the inspectors' experience accuracy in picking out birds that were diseased with high sensitivity (finding and condemning birds that are diseased) and high specificity (not condemning birds that are healthy. If we assume that the inspector has the above characteristics due to comparable USDA training, then the emphasis will be on identifying diseased birds  $P(D)$  on the farm. Note that the assumption that inspectors have comparable knowledge may be questionable.

The function for the condemnation rate (CR) or probability of condemnation  $P(C)$  is:

$$CR = f\{P(D), P(I/D), P(I/L)\}$$

This determines the joint probability of condemnation at the plant. Note that if the  $P(D)$  is low, the CR will be low and this is the area of emphasis in flock testing.

## 5. THE RESEARCH DESIGN FOR FLOCK TESTING

5.1. Study Format-The Poultry Systems Approach: The study design utilized a systems concept, whereby a detailed evaluation of the determinants of population health were performed by systematically identifying and interrelating all variables which have biologically explainable influence on condemnation rates due to diseases. Environmental, managerial, as well as host and agent factors which may affect the incidence of poultry diseases and the condemnation rate

at slaughter plants, were scrutinized via casual diagrams and multivariate epidemiologic models designed for possible predictive and/or discriminative purposes. Since poultry (broiler) production involves a sequentially predetermined set of factors which include breeder flock sources, hatching, brooding, growing and processing, the identifications of all potentially useful predictors of the condemnation rate at slaughter were integral parts of this research; designed to take the total poultry production ecosystem into consideration.

5.2. Procedure for Identification of Variables: The complete list of original variables for which data were sought are provided in Appendicies 1 and 2.

5.2.1 The hatchery subsystem: The first task was to identify the variables which operate in the hatcheries and had a potential causal influence on condemnation rates (figure 5). In this and subsequent diagrams, dotted lines indicate the paths of causal factors which may influence the population (state variables) to become infected, e.g. sanitation affects the population and type of microflora in a hatcher, which may in turn affect the rate of infection in the hatched chicks. The bold lines indicate material transfer from one state to another, e.g. eggs obtained from breeder flock sources are set in incubators. The fertile ones are hatched, then transferred to brooder houses. The circles represent auxillary variables which have an influence on state variables represented by rectangles, e.g. in the



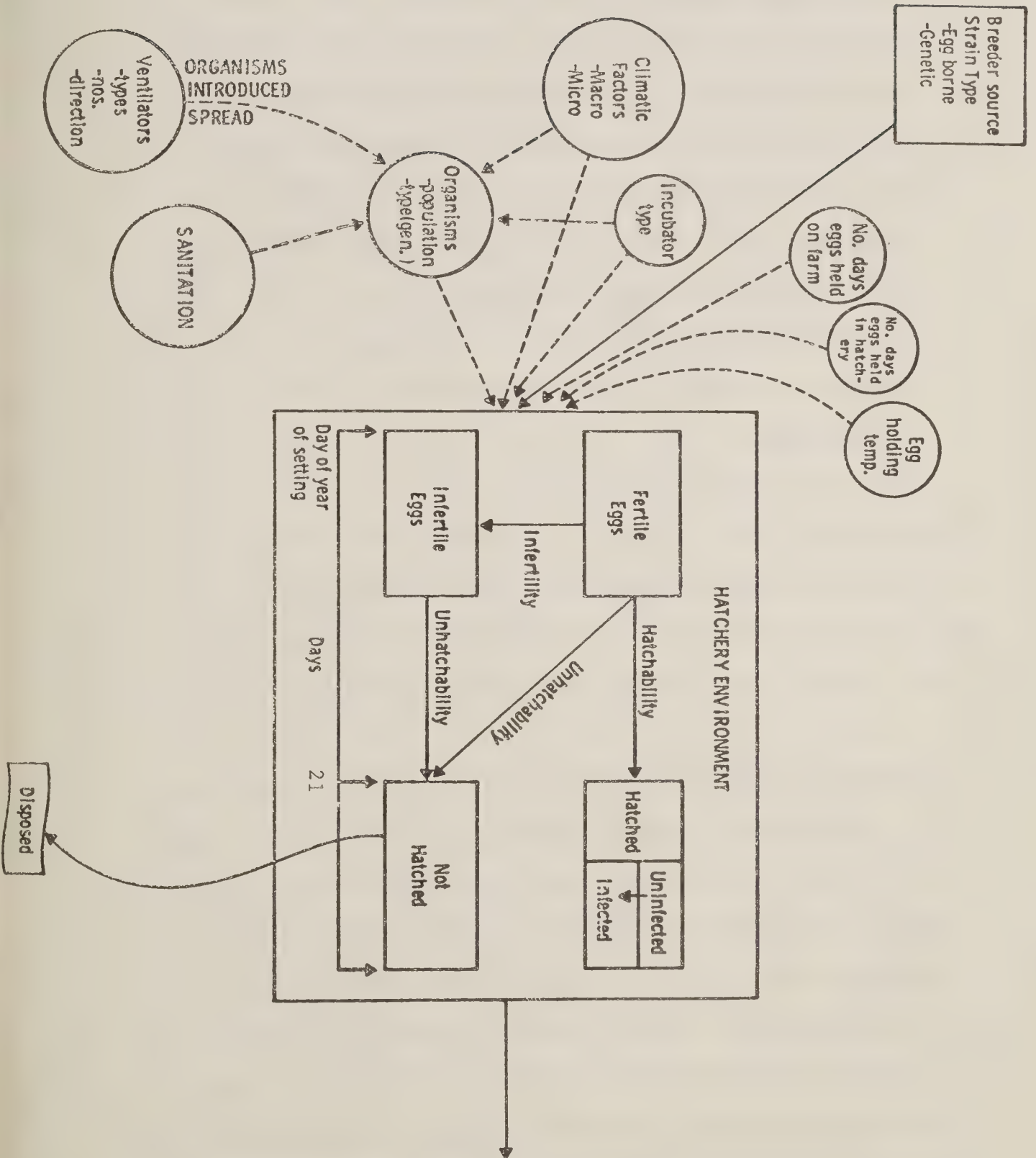


Fig. 5 THE HATCHERY SUBSYSTEM

hatchery there are two state variables representing fertile and infertile eggs in the setter. From this point on, those fertile eggs which hatched transit to two states, viz infected or uninfected chicks. The infertile and unhatched ones are discarded. The infection in the hatchery may arise via genetic or egg-borne transmission (from breeder flock), or as a result of exposure to various disease factors and infectious agents in the hatchery as indicated in figure 5. Note that the transitions from fertile to hatched are sequential events that take place in the hatchery, and these transitions could have rates such as fertility, hatchability.

The most important areas to examine are the variables (circles and the dotted lines) that originate from or lead to such areas; these provide the clues to the causal influences on population health which eventually influence condemnation rates further down the line. The variables identified via this figure were:

- Hatchery Source (Variable codes  $X_{57}$ ,  $X_{58}$ ,  $X_{59}$ ,  $X_{260}$ ,  $X_{261}$ ,  $X_{262}$ ,  $X_{263}$ ). There were 8 hatcheries which provide baby chicks to the study farms in this project. Each of these were separate entities with different management practice so that variabilities do exist in the source of hatched chicks for broiler production. Since the hatchery source was a categorical or nominal variable, it was not possible to quantitate it directly. There will be others like this, so it is important to note how one establishes an indicator or dummy variable for such

cases. Using hatchery 1 ( $X_{57}$ ) as an example:

$X_{57} = 1$  if chicks came from hatchery 1,

0 if chicks did not come from hatchery 1.

Thus any time the source for baby chicks was hatchery 1, a value of 1 is given to variable  $X_{57}$  and 0 assigned to others. In general, when establishing such indicator variables, the rule is to use one less than the actual number of nominal variables (49). In this case then, since baby chicks were obtained from any one or two of the hatcheries and since there were eight hatcheries, the total number of dummy variables established were seven.

- Type of incubator ( $X_{60}, X_{61}$ )- There were two major types of incubators in use, viz, Chickmaster and Big J, with a few "other" types. Again, since this was nominal data, three categories (Chickmaster, Big J., others) were set up and two indicator variables were created.
- Ventilation is an important area, and what is taken into consideration is the type of ventilators ( $X_{20}, X_{21}, Z_4$ ) and the number of ventilators ( $X_{22}$ ). Three categories of ventilator types (3 CFM, 5 CFM, and others) were established and two dummy variables were created. Location of air intakes ( $X_{256}, X_{23}-X_{25}, Z_5$ ) and exhausts ( $X_{257}, X_{26}-X_{28}, Z_6$ ) were all nominal variables with 5 levels (directions) for each. The directions considered were: roof, east northeast, north northwest, west southwest, and south southeast. An appropriate number of dummy variables were then established. Note that ventilation is important either in introducing microbial agents from outside, or

spreading the ones already in the hatchery or poultry house.

The information on ventilation was obtained from observation of hatcheries.

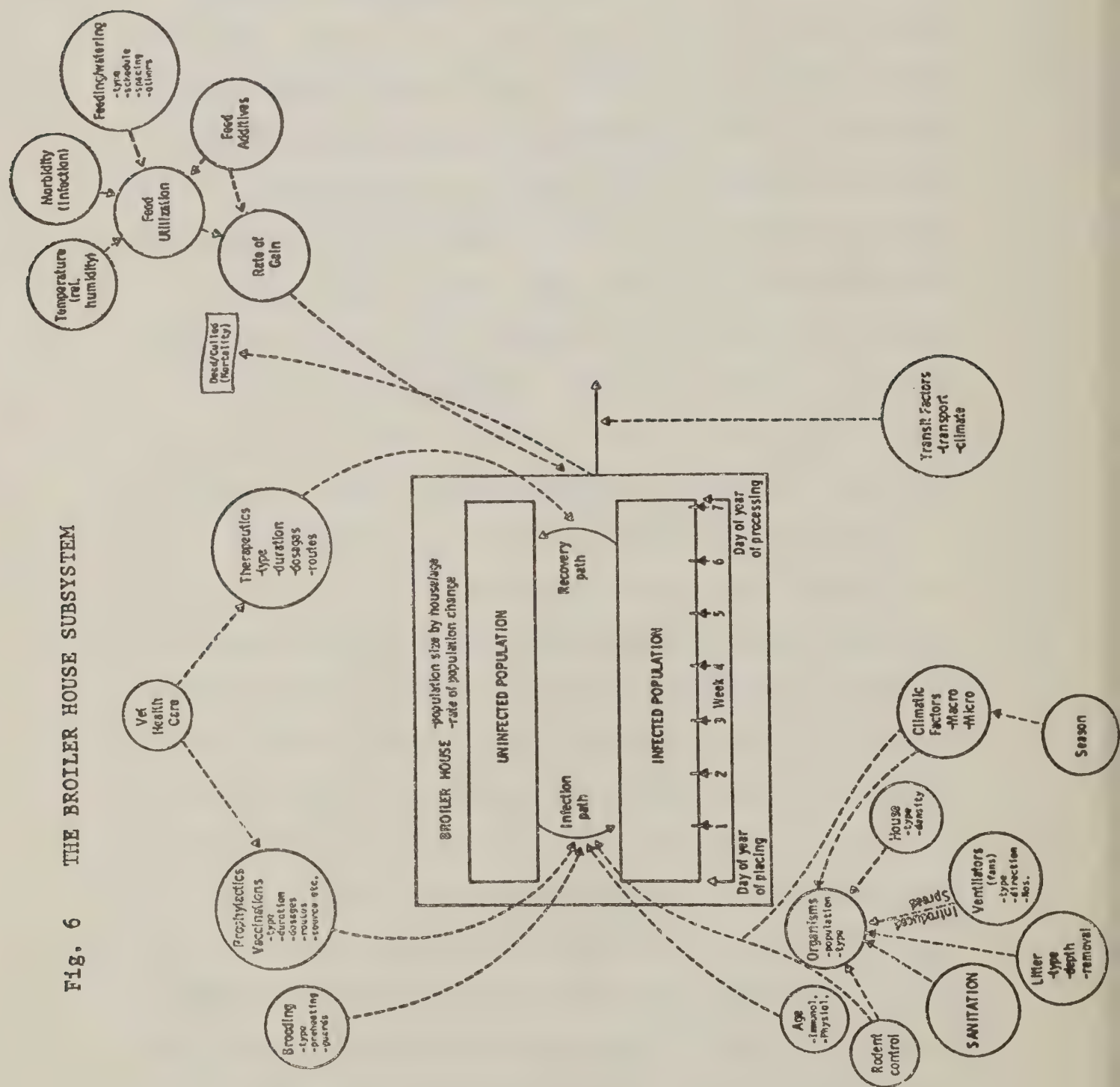
- Sanitation assessment of hatchery ( $X_{74}$ )- This was another type of variable which was difficult to quantify directly. It was a composite index made up of various categories. To quantitate this data in a somewhat objective manner, and to make it useful, six criteria were established. Each hatchery was graded on a scale of 1-3 with one being "good", 2 representing "average" and 3 for "poor" or "unsatisfactory". The criteria were: offensive odor, dustiness, cobwebs on walls/ceilings, freedom from garbage and refuse, availability of waste disposal within easy reach or sight, and unwashed (unsanitary) equipments/areas. Based on a grade for each of the six criteria, a final "average" grade referred to as the sanitation index was computed. Thus, this variable was one which was ranked based on specified criteria. Note that ranking is another established quantitative technique in handling nonnumerical data as in the case of nominal variables (49).
- A set of directly quantifiable variables for which numerical values were available for, were also identified. Only the variable codes were given here and one could easily refer to data collection form 1 and obtain a description of what these variables were. These were  $X_{62}$  -  $X_{72}$  and  $X_{77}$ . The information about these variables were gathered from regular visits to hatcheries.
- Another set of variables closely associated with hatchery data



were those pertaining to breeder flock sources and major strain of birds. Four levels for the major strain of birds (and the breeder source) in Alabama were assigned for Corbett, Arbor Acres, Peterson, and "others". This was based on prior information on the major groups of breeding stock in the state. Again, breed/strain was nominal data and appropriate dummy variables ( $X_8$ ,  $X_9$ ,  $X_{10}$ ) were set up according to the method described earlier. By establishing these variables for the strain of birds, it also automatically took care of the breeder flock sources since these sources basically specialized in producing only certain strains of birds. Other quantifiable data, such as  $X_{14}$  and  $X_{15}$  pertaining to the number of strains and breeder flock sources, were handled directly. Such data were obtained from visits of hatcheries.

- 5.2.2 The broiler house subsystem-brooding and growing- are the subsequent stages which follow hatching. Again, the birds are exposed to various risk factors in such a setting and epidemiologically relevant factors were identified with the aid of a systems diagram (Figure 6). The keys to the diagram were presented under hatching data. In this case, there were two major state variables, an uninfected and an infected subpopulation constituting the total broiler population in a given house or farm. The infected subpopulation arises as a result of exposure to risk factors while the birds are in the broiler houses. Of course the converse, that is transition from infected to recovered (uninfected), occurs as a result of therapeutic medications, while vaccinations, prophylactic

Fig. 6 THE BROILER HOUSE SUBSYSTEM



medications and other disease preventive programs maintain the portion of the uninfected subpopulation in that state. Again, the significant point was the identification of all potential variables which may influence the subpopulation of uninfected, to transit to the state of being infected. The variables so identified were:

- Population descriptive variables - included in this category were initial flock size ( $X_3$ ) and the flock size at time of processing ( $X_{222}$ ), and estimated proportion of under sized birds in the population ( $X_7$ ). These variables were directly quantifiable and were gathered during visits to the growers.
- Housing - the type and area (density) available for the flock was considered. In terms of house type, three categories were established for type 1 (conventional/fan =  $X_{16}$ ), type 2 (conventional/no fan =  $X_{17}$ ), and type 3 (others). Since these were nominal variables, two dummy variables were set up accordingly. The second aspect of housing was population density per square foot ( $X_{18}$ ), which was directly quantifiable from available data.
- Ventilation - type and the direction that the intake and exhausts face is important in introducing microbial agents from external sources and/or spreading them within poultry houses. The air intake variables considered were ( $X_{264}$ ,  $X_{78}$ - $X_{80}$ ,  $Z_{10}$ ). The corresponding air exhaust direction variables were ( $X_{265}$ ,  $X_{81}$ - $X_{83}$ ,  $Z_{11}$ ). The respective directions were roof, east north east, north north west, west south west, and south south east. The appropriate data were obtained from field observation of the

broiler houses.

- Sanitation index for broiler farms ( $X_{186}$ ) was computed in a comparable manner as discussed under hatchery sanitation index. The assessment of sanitation was performed by the same two individuals who visited and graded the hatcheries. This way, a comparable type of data with less variability amongst observers was generated.
- Litter is related to housing, and included here were variables such as the type of litter ( $X_{189}$ , for shavings or sawdust), litter change for subsequent flocks ( $X_{192}$ , partial or complete), depth of litter ( $X_{190}$ ), interval between litter changes ( $X_{191}$ ) and number of batches of birds on the same litter ( $X_{194}$ ). The last three variables were directly quantifiable, while the first two were dichotomous and one dummy variable represented each of those. Other variables, such as procedures for house cleaning after litter removal and methods of removing litter, were also considered. Such data were obtained from growers.
- Management assessment criteria - as in the case for sanitation index, relatively objective criteria for ranking purposes were established for farm record keeping, cooperative attitude of farm personnel and overall farm organization and management. By grading on a scale of 1-3, an index of record keeping ( $X_{209}$ ), cooperation index ( $X_{211}$ ) and management index ( $X_{212}$ ) were established. These criteria are indirect measures and are somewhat subjective and thus limited, but data were gathered for possible descriptive use. Other management concerns such as farm security, and rodent control programs were also obtained



when available.

- Brooding variables - directly quantifiable data such as day of year of placing with day one for the year beginning January 1 ( $X_{85}$ ), number of chicks dead on arrival ( $X_{86}$ ), length of time (hours) for preheating of broiler house ( $X_{87}$ ), partial vs whole house brooding ( $X_{88}$ ), age (days) when brooder guards were removed ( $X_{90}$ ) and flock size per house ( $X_{91}$ ) were obtained from growers by requesting such information during scheduled farm visits.
- Macro and microclimatic data - more specifically, this referred to the macro temperatures (average maximum, average, average minimum temperatures) - ( $X_{202}$ - $X_{204}$ ), total precipitation ( $X_{205}$ ) and number of rainy days ( $Z_r$ ) per month, these affect the microclimate ( $X_{93}$ - $X_{96}$ ) in the broiler house. This information was obtained from the National Climatological Data Center (ref.). The data for the nearest weather station where study farms were located, was used for this purpose. It was not possible to obtain microclimatic data from broiler houses, in a regular basis, since growers neither keep such records, nor would they cooperate in keeping daily records on such data.
- Season - although season is a function of the climatic variables listed above and the study design takes this into consideration, season in itself was also used as an independent index with possible predictive power. Four levels of season (fall, winter, spring and summer) were designated by three dummy variables. They represented fall ( $X_{206}$ ), winter ( $X_{207}$ ) and spring ( $X_{208}$ ). Thus, the influence of season on a given brood of birds could be

captured in an approach which has been utilized in similar fashions in other fields (50).

- Morbidity indicators - as given in figure 5, the number of infected birds divided by the total population on a given farm or house represents the morbidity rate, which directly leads to infected birds being slaughtered. However, the morbidity rate of the subpopulation of birds that may have been infected were difficult to identify. Data of morbidity were unavailable from growers and company records. Thus, various indirect measures of morbidity were devised to assess this vital information. The indirect indicators used in this study were:

- mortality data obtained from existing farm records
- serological profiling
- necropsy profiling and
- feed utilization

Except for mortality, data of the rest of the above indicators were gathered from field for laboratory studies by the research team, and these represented a major portion of the field work. These last three items will be discussed in greater detail further into the report. With respect to farm mortality data, reasonably accurate weekly mortality records were available although the cause of mortality by specific disease were unavailable. Mortality rate on farm ( $X_{30}$ ) and more specifically, age specific mortality rate at 4 weeks of age ( $X_{39}$ ) and at 7 weeks of age ( $X_{40}$ ) were computed using the formula:

$X = \frac{\text{total number of birds dead by 4 or 7 weeks on farm (house)}}{\text{total population on farm (house)}}$

average population at risk on farm (house) during same period

Where X is  $X_{39}$  or  $X_{40}$ .

In addition, specific mortality rate in a house ( $X_{31}-X_{33}$ ,  $X_{258}$ ) was also utilized as a predictive variable. It is important to note that mortality data in itself is not a very useful indicator for condemnation rate since the birds are already dead and never reach the processing stage, but the assumption is that other than mortality due to non-disease causes, those deaths that occur as a result of infection, may be correlated with morbidity in the population. The relationship is not so much with morbidity, but with case fatality. This is so because there could be a chronic infection which may not result in the death of the bird but may eventually be the cause for condemnations at the time of processing.

- Microbial profile data - It is vital to see how the research design utilized indirect measurements of the population morbidity rate to correlate with condemnation rates. If one examined both areas carefully, it can be recognized that many variables, directly or indirectly, affect either the population and/or the types of microflora in the hatchery or broiler house subsystems which pose risks of infection in susceptible birds. For example, in the hatchery, factors pertaining to sanitation, ventilation, climate and type of incubator all affect the microbial flora, which in turn poses the risk of infection for newly hatched chicks. In the broiler subsystem of the diagram, such factors as rodent control, sanitation, litter, ventilation,

housing and climate determine the type and population of micro-organisms in broiler houses.

The high density of birds in large poultry production units increases the possibility of disease spreading through airborne microroganisms, dust and air contaminants. Therefore environmental quality control and the collection of information concerning airborne bacteria and fungi in poultry establishments becomes crucial. Data concerning the overall population of organisms and of their type, specifically on their pathogenicity and/or toxin producing potential, are useful (18, 46).



The research design emphasized the need for obtaining a microbial profile of the flora in hatcheries and poultry houses; these were respectively referred to as variables  $X_{100}$  to  $X_{102}$  for the population size of bacteria and fungus in randomly selected air samples from poultry establishments. Additionally, because of the need to identify the types of microbial organisms in the air samples, the variables designated  $X_{103}$  -  $X_{107}$  were created. Although it was recognized that microbial profiling (quantitating the population and identifying the types of organisms) was essential in establishing the link of factors that affect poultry health (Figures 5, 6) due to limited financial supports and lack of semiautomated equipment, to handle the large column of samples collected, bacterial and fungal agents picked up from hatcheries and poultry farms were identified only for a few study farms.

- Medication - Veterinary health care, (therapeutic and/or prophylactic medications), plays an important role in determining morbidity and mortality rates in poultry (Figure 6). The specific variables identified with potential influence on morbidity and mortality were types of medication, duration of administration of medication, dosages and routes of administration.

Both therapeutic and prophylactic medications contain the variables named  $X_{138} - X_{163}$  and  $Z_{14} - Z_{17}$ .

- Vaccination - in the systems diagram (figure 6), prophylactic medications and vaccinations were placed together in one category, because both are disease preventive programs intended to minimize the transition path from an uninfected state to an infected state. In terms of vaccination data, the variables for this study include vaccine manufacturers ( $X_{169} - X_{171}, Z_{19}$ ), route of vaccination ( $X_{172}, X_{173}, Z_{20}$ ), vaccination schedule ( $X_{174} - X_{179}, Z_{21}$ ) type of vaccine ( $X_{181}, X_{182}, Z_{22}$  and degree of adverse reaction to the vaccine ( $X_{184} - X_{185}$ ). Most of these variables were categorical and appropriate indicator variables were set up to quantitate them.
- Feed utilization - as one of the indirect health status indicators in a population, feed utilization occupied an important part in this study (figure 6). Feed utilization of birds is affected by such variables as ambient temperature, feeding/watering practices, (type, spacing, scheduled vs ad libitum feeding) administration of additives and above all, morbidity or prevalence of infections in the flock. Conversely, feed utilization affects rate of weight gain, which in turn reflects the health of the

flock, including morbidity.

Because of the importance of feed utilization data in providing clues to the morbidity rate on a farm, a detailed listing of variables from type of feed ( $X_{116}$ ,  $X_{117}$ ), feeding ( $X_{119}$ ) or watering ( $X_{129}$ ) space to a procedure for collecting data establishing weekly feed utilization and the rate of weight gain, was designed ( $X_{132}$  -  $X_{135}$ ). Some of the variables were nominal in nature, while others were directly quantifiable.

5.2.3 The transit and processing system: The third stage in the sequence of poultry production phases which were evaluated via a systems approach were factors affecting condemnation of poultry due to transit or those that arose while birds were being processed (figure 7). This is similar to figure 4, except that in-transit factors have been added and the figure expanded further to focus on condemnations. Although it has been pointed out earlier that an infection must have necessarily arisen while birds were on the farm for it to have enough time to reach the stage of lesion development, other factors which may have some influence on condemnations such as transit stress including: distance from farm to plant ( $X_{223}$ ), number of hours of driving from farm to plant ( $X_{224}$ ), drivers and trucks involved ( $X_{225}$  -  $X_{228}$ ), types of coops used ( $X_{229}$ ) and population density per coop ( $X_{230}$ ) and per truck ( $X_{231}$ ), method of cooling birds in processing plant ( $X_{234}$ ) and

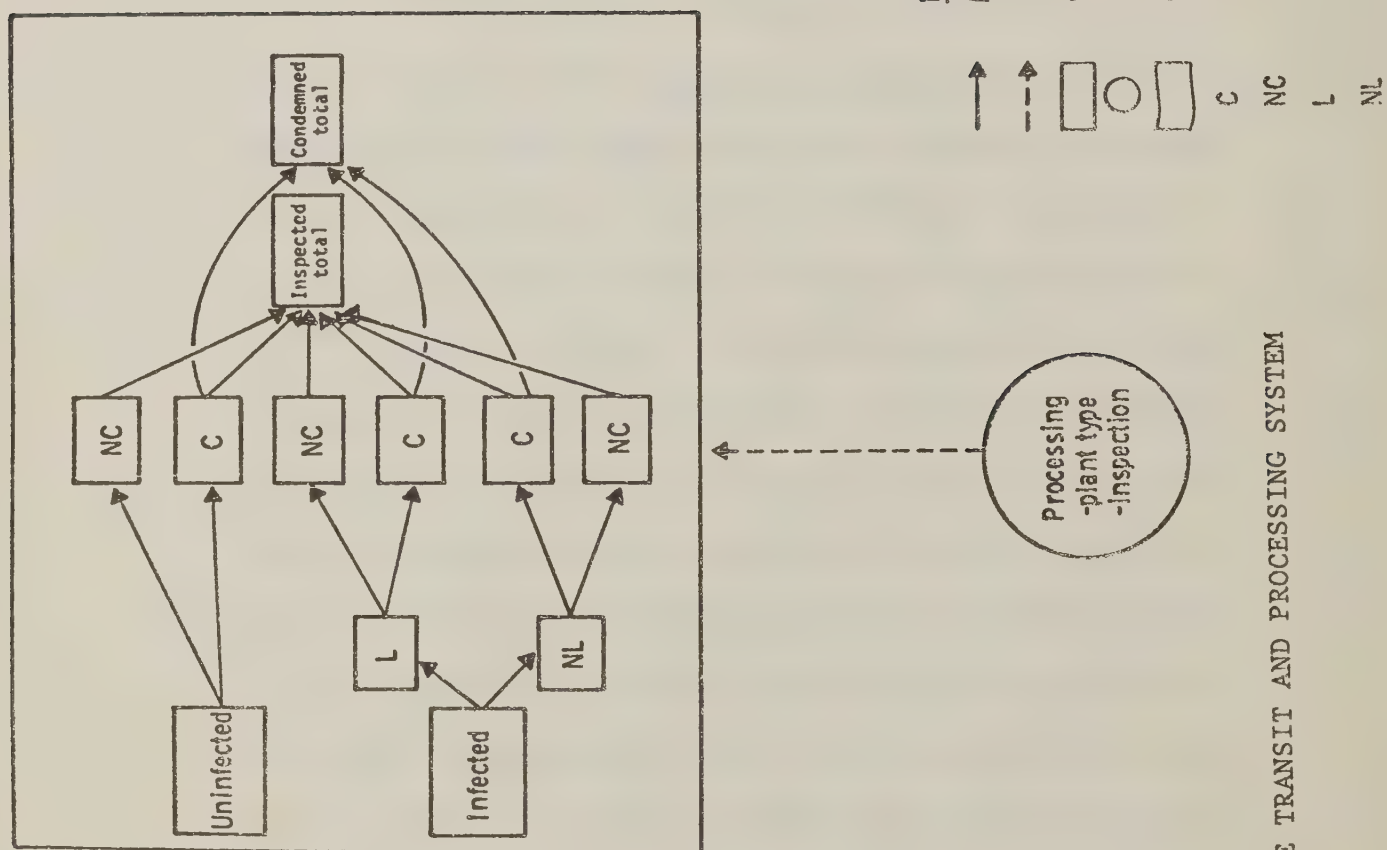


Fig. 7 THE TRANSIT AND PROCESSING SYSTEM



macroclimate on date of processing ( $X_{238} - X_{240}$ ) were also considered. Some of these data were nominal, while others were directly quantifiable and the methods used to establish values for the nominal data were the same as given in earlier sections. The most important aspect of this last segment was that data on condemnations due to diseases and other causes ( $Y_2 - Y_{17}$ ), which served as the dependent variables, were also collected at this time. Such data were provided by management of the plant upon completion of the condemnation report by the inspector in charge. The same categories for causes of condemnation due to diseases (FSIS reports) were used in the data collection forms (appendix 2).

In addition to condemnations due to diseases, data on total number of pounds (lbs) of parts trimmed and non-disease condemnations were also obtained. Additional data on condemnation for birds on all farms processed in that plant on the day that birds on study farm were processed, obtained for comparative purposes. From these data, the condemnation rate due to disease for the study farm ( $Y_2$ ) was computed using the formula:

$$Y_2 = \frac{\text{Total number of study farm birds (whole carcass) condemned due to diseases}}{\text{Total number of study farm birds inspected}}$$

Disease specific condemnation rates of birds on study farms were also computed for the following diseases: leucosis ( $Y_9$ ), septicemia-toxemia ( $Y_{10}$ ), airsacculitis ( $Y_{11}$ ), synovitis ( $Y_{12}$ ), tumors ( $Y_{13}$ ), and others ( $Y_{14}$ ). These disease specific rates were computed from formula:

$$Y = \frac{\text{Number of study farm birds condemned due to specific disease}}{\text{Total number of study farm birds inspected}}$$

Where Y = disease specific rate.

Note that since these were the dependent variables, the code names begin with Y while all other possible predictor or explanatory variable names were coded as X's. One other variable of importance was the condemnation rate for the study farm at one previous brood, referred to as  $Y_{t-1}$  (Y at t-1 period, or condemnation rate at one previous brood), which was used as a historical reference variable for predictive purposes. This is based on the rationale that the performance of a poultry grower may in fact be judged by how one performed or managed at previous times, i.e. based on experience or historical performance.

Since the systematic examination and identification of variables with potential predictive value have now reached the end point of the poultry production process, a more

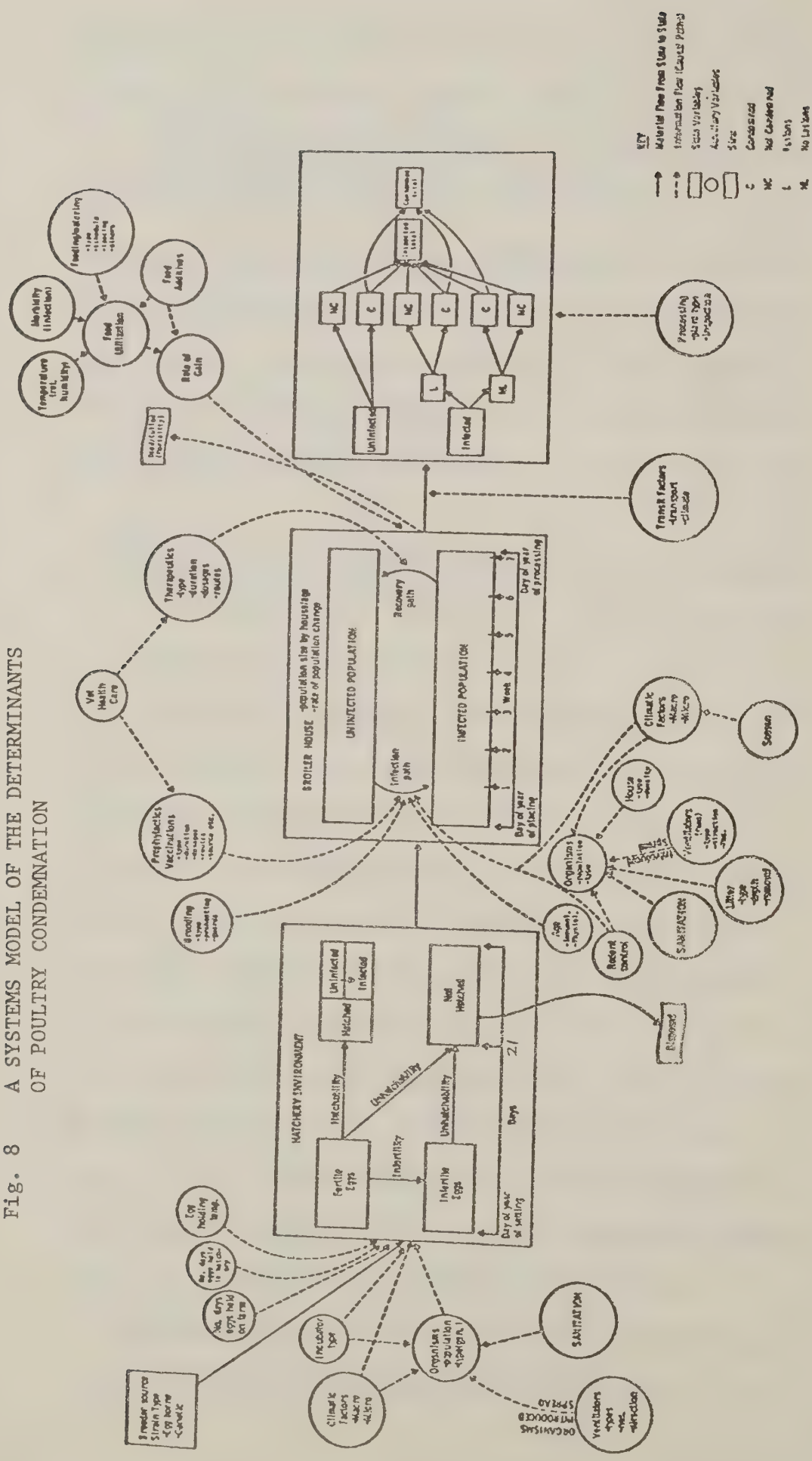
holistic systems diagram of the poultry exosystem and its determinants as there affecting condemnation of poultry is presented (figure 8). The various segments of this diagram have already been discussed, so what is shown here should be self explanatory in providing one with the total conceptual and design framework for analyzing the data generated from such a model.

NOTE: The complete list of original variables identified from the hatchery, broiler house, transit, and processing subsystems are in appendices 1 and 2.

5.3. Study Unit: Based on pilot studies to determine where adequate data could be collected from an individual poultry farm was initially considered the study unit. However, the original design specified data collection from a farm on a house by house basis too whenever possible. The major problem to collecting the data on a house basis was that data for the dependent variable (condemnation) on a house basis at the slaughtering plant was unavailable. Later, by prior arrangements with the management of each cooperating firm and inspector in charge of the processing plants, birds were processed and data recorded on a house basis. Therefore, both the house and farm served as two experimental units.

5.3.1 Sample selection: Having identified what the experimental unit was, five poultry companies in Alabama was selected for the study. Originally, a letter was sent out to nine firms in Alabama. Only four firms responded to the

Fig. 8 A SYSTEMS MODEL OF THE DETERMINANTS OF POULTRY CONDEMNATION





request for cooperation in this study, and personal visits and discussions held with officials of these four firms. Only three firms were willing to cooperate in this study. However, with more assistance from Dr. Edgar and FSIS, two more firms eventually participated in the project. The selection criteria for experimental units (farm/house) from each of the five firms consisted of identifying cooperative growers within reasonable driving distance of each other. Thus, the question of cooperation and logistics was vital as opposed to the originally planned method of random sampling of farms.

5.3.2 Stratification of sampling units: To ensure a representative cross section of farms, the study farms were stratified across three strata, of good, average and poor production performance based on the criteria for classifying a grower in one of these categories. The criteria for ranking growers varied from firm to firm as presented below:

Procedures for ranking grower performance for firm 1: The growers were ranked both weekly and annually. For weekly ranking, all growers that had birds processed in a specific week were compared to one another via an index of performance criteria to be presented below. Annually, the farms were ranked on production costs.

The fixed cost factors considered were: cost per baby chick, cost per ton of feed, cost of vaccination, de-beaking cost, and overhead and service costs.

The variable cost factors were: sanitation costs (wash water, cleaning area around chicken house), and medication costs (depends on type of drug and duration of usage).

The total cost of producing the flock divided by the total pounds of birds processed resulted in the cost for a pound of meat which was the criteria for ranking growers as: good, average or poor. Growers with the highest production cost were ranked, "poor". Those with the least production cost were ranked, "good", and the rest were rated as average.

Procedures for ranking grower performance for firm 2: The growers were ranked weekly and annually in a comparable manner as described for firm 1.

The fixed cost factors considered were: cost per baby chick, and cost per ton of feed.

The variable cost involves medication and other costs. Again, the cost items were summed and cost per pound of meat computed as in firm 1. Ranking was assigned accordingly.

Procedures for ranking grower performance for firm 3: The growers in this firm were ranked weekly through a computerized system of accounting. There were three categories viz. above average, average, below average.

The fixed cost factors considered were: baby chick cost, feed cost, and service and overhead cost.

The variable cost factors were: medication cost, and miscellaneous cost.

The above cost items were summed to obtain the total cost. The firm then considered three indices: the average live weight that birds should attain was set at 3.85 pounds, attain the least amount of feed consumed to produce a pound of meat, and cost due to condemnation loss computed from the report of IIC.

The farm production cost plus the loss due to condemnations were combined to derive the grower's cost. The grower's cost for a certain week were summed and this total cost was then divided by the number of growers to arrive at the average growers cost. If an individual grower's cost was higher than the average grower's cost, he/she would be ranked, "below average". If the cost was lower, the individual grower was ranked, "above average".

Procedures for ranking grower performance for firm 4: The growers were placed in one of three categories monthly through a computerized system. The formula for ranking growers is an adjusted feed conversion index which was derived from the average live weight of birds + a standard weight of 3.67 lbs. For example, if a grower produced an average weight of 4.12 lbs broilers and had a feed conversion index of 2.07, therefore, the adjusted feed conversion would be:  $4.12 - 3.67 = 0.45$  lbs.

The above value was then divided by 5, an arbitrary fixed value of 0.09 lbs was obtained. One then subtracted 0.09 lbs from the original feed conversion index, of 2.07 lbs., to arrive at the final adjusted feed conversion index for

the grower, which in this case would be 1.98 lbs. of feed for one lb. of meat. In this ranking procedure, the lowest adjusted feed conversion index is the best while the highest corresponded to a poor rank.

Procedures for ranking grower performance for firm 5:

Growers were placed in one of the three categories in association with production costs. The fixed cost factors were: cost per chick and cost per ton of feed.

The only variable cost factor was medication.

The total production costs of per pound of marketable meat was computed for each grower after their birds were processed. The average production cost for all farms with birds processed in a certain week, was obtained by dividing the total production cost by total pounds of marketable meat after condemnation. If an individual grower's production cost was higher than average, a minus (-) factor would be assigned to him; if the production cost was lower than average, a plus (+) factor would be assigned. These cost figures were calculated for each grower after each processing of each brood of birds and also annually.

The annual production cost was derived by dividing the total production cost for the year by the number of broods. To encourage lower production cost, a prize was given to the grower with the lowest production cost for the year. Using the criteria for the selection of study units from each firm, at least two growers were selected



from each strata. This decision was made to ensure that at least one grower would represent each strata in case some of them decided to withdraw from the study for reasons beyond the control of the research team. If all selected growers continued to stay in the project, this would expand and strengthen the data base.

One major adjustment was made at the end of August, 1981. to reduce the total number of study farms per firm from 6-7 down to 3-4. This adjustment was necessitated as a result of a reduction in the number of student research assistants who were working on full time basis during the summer, but had to go back to school in early September. Thus, the practice of fielding two or three teams concurrently to collect data was not possible.

Although the number of study farms were reduced to three or four, the criteria for selection of which farm to drop and which to retain was based on:

- maintaining representation of good, average and poor farm rankings as described earlier
- keeping the farms where the growers were most cooperative in providing detailed data regularly collected at four or seven weeks

The final make up of the study farms consisted of four farms from firm 1(A), four farms from firm 2(B), three farms from firm 3(D), four farms from firm 4(E), and five farms from firm 5(F). Therefore, there were a total of 20 study farms which consisted of 40 houses. Although there were potentially 40 sets of observations, from each experimental unit (house) during any one brood cycle, one firm (D) did not provide

condemnation data on a house basis.

### 5.3.3 Sampling time frames: Two type were followed:

- a. Sequential or longitudinal follow-up which involved:
  - examining the health status of the population and its different determinants at various cross-sections in time for a group of cohorts.
  - collecting data on the appropriately identified multivariabls from farms during early, middle and later stages of a growout.
  - collecting corresponding condemnation data on the same cohorts from processing plants.
- b. Cross-sectional sampling:
  - conducted at one cross-section in time to provide a measure of prevalence of the specific determinants within the specified farm ecosystem.
  - multivariable data collected from the farm before birds were shipped to slaughter and then obtaining the corresponding condemnation data from the processing plant.

In essence, these were specified sample data collection time frames from a hatchery, broiler operation and processing plant (figure 9). Using these sampling time frames, data were collected during one complete year (5 brood cycles) to accomodate possible seasonal and other time related variables.

### 5.3.4 Sample data collection: by definition, a cohort of birds

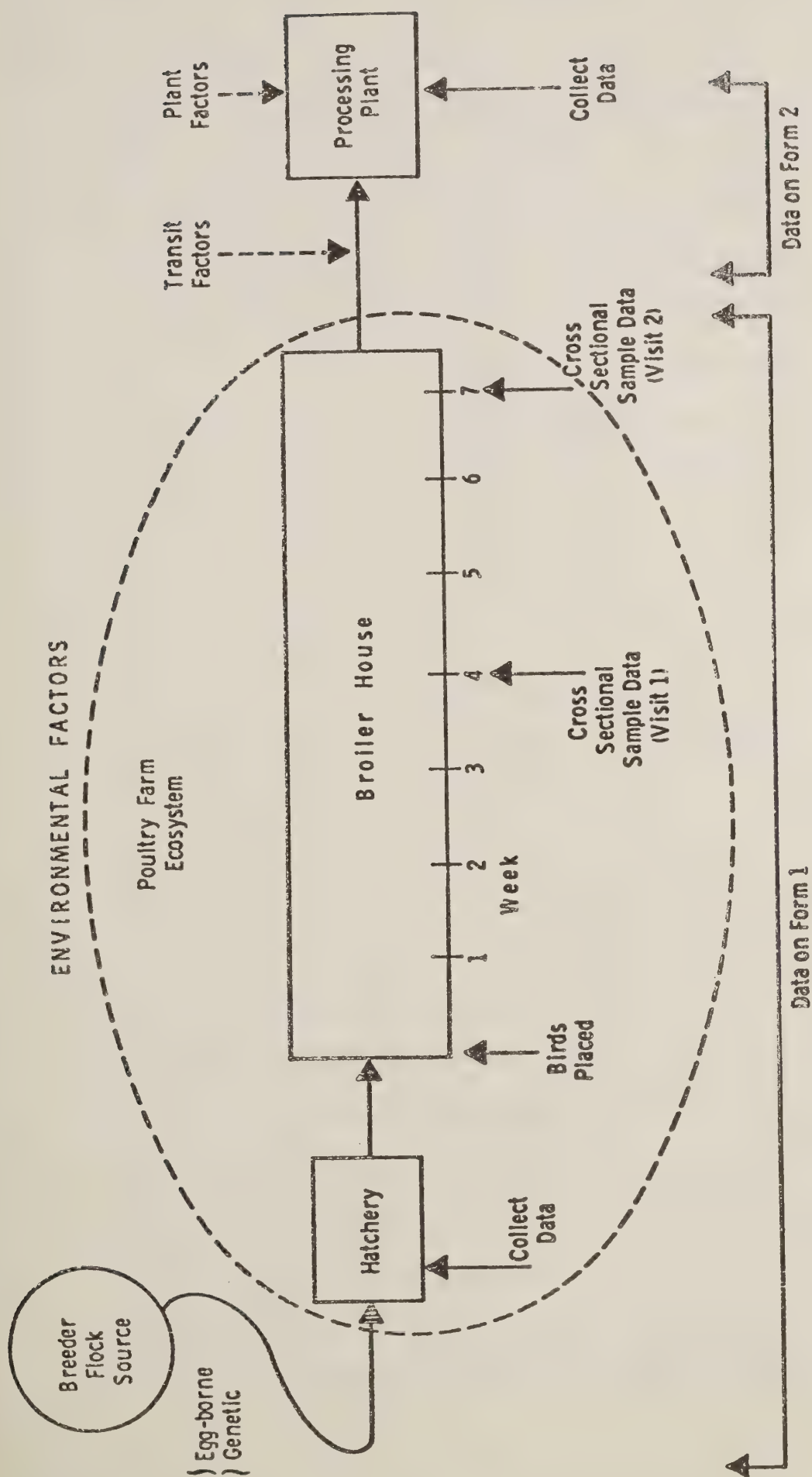


Fig. 9 FLOCK TESTING FEASIBILITY STUDY - CONCEPTUAL FRAMEWORK

that were sequentially monitored to collect data from each of the three phases of broiler operation (hatchery, broiler farm, processing plant), was referred to as one brood cycle. It requires approximately 50 days to raise a bird to the desirable marketing weight as a broiler. Such a data collection time frame was projected to take place for a period of one year. The first visit involved the hatchery, with specific goals to:

- assess the sanitation index for the hatchery
- obtain air samples from randomly selected sites in the hatchery as well as from the hatcher where chicks were scheduled to be sent to one of the study farms.
- collect preexisting hatchery data

Subsequent to collecting hatchery data, each study farm was visited during the first week that birds were placed on the farm. During this time, air samples were obtained for microbial profiling to provide information on the potential infection causing factors in the brooder houses. During the first week of life, baby chicks are most susceptible to infection, therefore the microbial sampling of farms was performed at that time.

Each farm was then visited at two different times; one when a given brood of birds were about four weeks old (visit 1) and again when they were about six to seven weeks old (visit 2). Note that, as given in the sampling time frames and as indicated in figure 9, a cohort of



birds were followed up from the hatchery through the growout period.

4-Week-Data (Visit 1): The data concerning flock history and different variables were obtained on about the 28th day, following placement of the chicks in the broiler houses, by questioning the grower and studying the performance charts in the chicken houses. A questionnaire (Form 1) concerning the variables mentioned previously was filled out by the visiting research assistants. At the same time, ten chickens per house were randomly selected and bled. The sera were transported to Tuskegee Institute for serological tests.

7-Week-Data (Visit 2): These data were usually obtained on about the 49th day, following placement of chicks in the broiler house. Form 1 was completed for this time period with all available information.

The final phase of the sample data collection time frame was that of obtaining condemnation data of study flocks from the processing plants, and the information was stored in Form 2. Later on in the report, this task will be discussed in greater detail. In addition to the sampling time frames, figure 9 presents the type of data collection forms to use and where. For example, all farm data were filled out on form 1 while processing data were filled out on form 2. The design of the data capturing format in this study has been an important aspect of the research development phase and will be presented in the

pages to come.

#### 5.4. Types of Data

There were three main types of data in this study.

##### 5.4.1 Preexisting data - e.g. condemnation rate at processing

( $Y_2$ ), weekly mortality rate from records kept by the grower ( $X_{39}$ ), etc. In such cases, the data were collected from existing records either on the farm or in the processing plants, and the quantitative values of the variables were incorporated with the corresponding set of data in a multivariate setting, both in terms of time and place.

##### 5.4.2 Field generated data - two subcategories were considered here.

- a. Data generated from field observations, e.g. sanitation index ( $X_{186}$ ), management variables ( $X_{212}$ ), etc. Research assistants of this project assessed the respective cases and provided quantitative estimates (numerical values) for the variables under study.
- b. Data generated from field measurements - e.g. the weight of birds ( $X_2$ ), the proportion of undersized birds ( $X_7$ ), the weekly feed utilization, etc. In these cases, actual measurements, e.g. counting undersized birds in a sample of 100 birds, weighing a few randomly selected birds, or measuring feed bins to estimate weekly feed utilization, were performed to generate data. An important part of

this task was data collection on weekly feed

utilization; a detailed description of which follows:

Feed utilization data collection procedure: Three farms from each cooperating firm (one good, one average and one poor) were monitored for feed utilization. These farms were visited once a week when possible. The level of the feed in each feed bin was estimated, compared to the level of the previous week. This provided the volume of displacement, which was converted into pounds of feed. If the level was higher than the previous week, it was assumed that additional feed must have been delivered. In some cases the growers kept the feed delivery tickets, from which the amount of feed delivered and the date of delivery were recorded for calculations at a later date. On one farm, the feed that was actually weighed to measure the amount of feed was dispensed at a particular time. This again, varied with the size of the birds and the temperature inside the chicken house.

The method for estimating the amount of feed in feed bins was indirect; the details of which are provided in appendix 3. Based on the method described, an estimate of the amount of feed consumed per bird per week was computed for a limited number of flocks with adequate information.

#### 5.4.3 Laboratory generated data:

##### a. Sample collection for serological and necropsy

profiling: An important aspect of the study design was the sampling of a representative number of birds

from the study farms for serological and necropsy examination. As referred to earlier, the study farms were selected by stratifying representation from good, average and poor production performance farm groups based on information provided to us by the respective cooperating firms. Although there was some stratification across three production strata, there was no random sampling of farms from each strata.

The importance of these parameters is primarily, for providing indirect measures of morbidity. As pointed out earlier (figure 6, 7), since morbidity data are difficult to obtain, and since most infected birds are eventually condemned upon processing, some mechanism of obtaining prevalence data on a given population of birds immediately before slaughtering could prove to be the most important piece of information in predicting condemnation.

It was with this background that serological and necropsy profiles of a flock of birds was studied since both parameters could possibly be adequate indicators of morbidity.

Serum Samples Collection Procedure: From each of the study units, blood samples were obtained at two stages during a brood cycle. The first stage samples were collected at four week of age from ten randomly selected birds per house.

Bleeding Procedure: A 1cc hypodermic syringe with a 26 guage 1/2" needle was used to collect blood from the



subclavian vein under the wing of the birds. The blood was then slowly forced out of the syringe into a 5cc test tube. A cap was placed on the tube to prevent contamination and spillage. The samples were transported to Tuskegee Institute, where the serum was separated from blood cells by centrifugation (2,000 rpm for 10 minutes) and stored at  $-70^{\circ}\text{C}$  in a serum bank until serological analysis were performed.

The second stage sampling of sera was done at the slaughter plant when the birds were being processed at approximately seven weeks of age. Blood samples were obtained from birds after the jugular veins were cut and were being bled out. Approximately four ml of blood was obtained from randomly selected birds, as described under the sampling procedure at processing plant. The blood samples were treated in a similar manner as in the first stage sampling. Sera from additional birds of the same flock were stored in the serum bank of the poultry Disease Research Laboratory, and will serve as future references. Three indicator diseases were tested in our laboratories by using the hemagglutination/hemagglutination inhibition (HA/HI) tests. These disease agents were Newcastle, Mycoplasma gallisepticum and Mycoplasma synoviae. A titer of 1:40 was used as the cut off point for positivity-negativity in the case of the mycoplasma, while a titer of 1:80 was used as a cutoff point for Newcastle disease. Since broilers were vaccinated with Newcastle disease

vaccine at an early age, a low titer of antibodies usually persist for some time and therefore a higher level of titer was used as the cutoff point as an indicator of infection.

During the first visit to the farm when the birds were about 4 weeks old, blood samples were collected from a randomly selected sample of 10 birds per house. From the processing plants, a predetermined sample size of 200 blood samples from each farm were collected for serological testing. Concurrently, 200 uneviscerated poultry carcass samples were also obtained randomly for necropsy profile studies.

Necropsy sampling: In order to randomly select 200 birds for necropsy sampling and blood testing, informations concerning the time required to process the study flocks, the line speed and number of birds being processed were acquired before processing was initiated. For example, if it required one hour (3600 seconds) to process a flock, to obtain 200 birds during that 1 hour period, the research assistants must pick up a bird every 18 seconds.

All necessary preparations were completed before the birds from study farms were processed. Insulated boxes with ice were placed at the sampling location. Blood sample collecting required one person, bird sample collecting required two people. A fourth person served as messenger to communicate between the back dock, sampling station and the inspection stations.

In collecting the sample birds, instead of using 18 second intervals, one used 15 seconds as the time interval, and picked the third bird that passed down the chute. The sampling was conducted on line right after the hock joints were cut. Approximately 20 birds were placed in an insulated cardboard imbedded with ice. Each box was properly marked to identify the grower's name, house number and processing date. At the end of processing, the boxes containing sample birds were re-iced and loaded onto a truck and taken back to Tuskegee Institute.

The necropsy profile ( $X_{109}$ ): The birds were usually necropsied and inspected a short time after arrival by the poultry pathologists associated with this project. Gross lesions were recorded in terms of specific conditions such as leukosis, septicemia-toxemia, airsacculitis, synovitis, tumors or others. The mere fact that the bird exhibited lesion of disease, whether mild or severe, was sufficient evidence for that carcass to be considered a positive case. The extent of lesions and parts affected are vital to decision making as to whether or not to condemn a carcass. In this case though, our necropsy efforts were not intended to make that decision, but to find out the prevalence of lesions which may or may not lead to whole bird condemnation in slaughtered birds.

Specific rates such as overall disease rate and specific disease rates were computed, using the total number of birds necropsied and inspected (approximately

200) as the denominator. The proportions ( or percentages) of diseased birds from each study farm were then utilized as one of the independent variables (specifically  $X_{109}$ ) to predict the overall condemnation rate for that study farm at processing. Also, more specifically, specific disease proportions ( $X_{110} - X_{115}$ ) were computed and utilized to predict the corresponding specific disease rates ( $Y_9 - Y_{14}$ ) at processing. (Appendic 1, 2). Data collection for  $X_{109}$  progressed through four brood cycles and had to be terminated thereafter.

b. Microbial profiling: In order to determine the effect microbial flora on condemnation of a specific flock, a limited microgial profiling study was conducted. Two aspects were involved in this process. Firstly, quantitative estimation of the microbial population was sought. The second aspect involved isolation and identification of microoganisms which occur in the hatchery and broiler house. Primary culture plates were prepared using standard bacteriologic technics. Initially three types of primary media were used; blood agar base for general bacterial culturing, McConkey agar for differentiating gram negative bacteria, and corn meal agar for fungi culturing. Since some bacteria do not grow in blood agar base alone, blood was added to the blood agar base in subsequent culture attempts.

The culture plates were placed in a bacterial incubator for 24 hours, to test for sterility, and only



sterile plates were used for bacterial culture.

Microbial sampling of the hatcheries: Culture plates were exposed to the air at different sites in the hatchery. In order to determine an optimal air exposure time, intervals of one, two, five, ten, and fifteen minutes were tried.

It was found that ten minutes exposure time was acceptable. After exposure, the culture plates were taped to avoid accidental exposure in transit and transported to the microbiology laboratory at Tuskegee Institute.

Microbial sampling of broiler houses: Upon placement of baby chicks in the broiler house, microbial samplings were performed within the first week of their life. Three sets of culture plates were exposed in three locations (at both ends and in the middle) of the chicken house, for one minute each (the exposure time was predetermined as acceptable, by a pilot study).

Bacterial and fungal colony counting: The samples from the hatchery and chicken house were incubated at 37 C for bacterial growth or were kept at room temperature for fungal growth. The number of bacterial and fungal colonies were counted, by using a Fisher Accu-Lite Colony Counter and recorded at 24, 48, and 72 hours. Since fungal colonies grow slowly, corn meal agar plates were kept for one week before discarding.

Identification of bacteria: Identification of bacteria collected from the study farms and hatcheries were not initiated until the latter part of this study due to lack

of funds.

Standard laboratory procedures were employed to identify the cultured bacterial colonies as described in "Diagnostic Procedures in Veterinary Microbiology" by Carter and Bergey's Manual of Determinative Bacteriology, 8th edition (52). The steps involved in this aspect of the work are presented in greater detail in Appendix 5.

In closing the section on research design, one should refer back to figure 8 to interrelate the significance of each variable, and grasp the holistic picture of its influence on the end result of predicting condemnation rates at processing. In that light, all existing data collected from hatcheries, farms and processing plants, as well as newly generated data from our laboratories and field work (microbial, serological, necropsy profiles, and feed utilization), should be viewed as occupying a specified causally identifiable position vis-a-vis condemnation rate at processing.

5.5. Data Collection Format: The design of a poultry health data collection format has been a much more complex and time consuming process than originally anticipated.

5.5.1 Basic requirements: The intention of developing such a form was:

- to be comprehensive enough to accommodate all epidemiologically relevant data pertaining to poultry health and management within the framework of the poultry farm ecosystem,
- to enable the collection of quantitative or numerical data for analysis, using multivariate techniques,
- to develop forms with the potential for serving as a standardized poultry health/management reporting format so that the data gathered could be computer coded, stored, retrieved and analyzed if a national or regional program were made operational,
- to provide relatively objective criteria to assess sanitation, management, farm security, rodent control, and record keeping.

The data base also allowed a retrospective review of data already collected, if such a need arose. For example, a format for disease outbreak investigation could be followed, and detailed data by house, age, strain, breeder source, hatchery, etc. could be examined to provide feedback to the grower and poultry firm if high

condemnation rates were encountered. Other additional data on health care and cost of the same have also been included.

5.5.2 Types of forms: With these objectives in mind, and after five lengthy revisions, the final two types of data collection forms were developed, (Appendices 1, 2).

Farm Data (form 1) - for collecting data from the farm environment, which included the hatchery and broiler houses. Such data were collected at least at two different times sequentially for the same brood of birds; when they were about four weeks of age and right before they were processed at about six-seven weeks of age.

Processing Plant Data (form 2) - for collecting corresponding processing and condemnation data from flocks for which farm data had been obtained.

Confidential Information Form - on this form, only the names of cooperating firms and farms were kept under strict confidentiality. The other forms bear only the codes of these farms and firms.

With the aid of these predesigned forms, all visits made by research assistants of this project and data generated from hatcheries, broiler houses and processing plants (figure 8) were filled in. This also meant that the logistics and scheduling of the field teams to gather such data at the correctly specified time was vital in obtaining valid and usable data.

5.6. Protocol for data collection: A descriptive protocol of



the research was prepared and distributed to all members of the research team. The protocol was self explanatory, with detailed descriptions, directions and examples where necessary. Tasks to be performed were planned and scheduled by the research associate, based on the implemented study design and routine managerial requirements. Major tasks to be performed during a given month were printed, and persons responsible for carrying out the tasks were assigned. Prescribed tasks were then carried out, following detailed weekly task schedules. A status report was filled out and followed by the research associate, as needed. In some cases, the tasks to be completed depended on the convenience of the study farm, and this was taken into consideration in planning and scheduling. Project staff meetings were held on Fridays to discuss and solve problems that arose. Changes of schedules, travel plans, expense accounting and communication were directed by the research associate before reaching the principal investigators.

## 5.7 Data handling:

5.7.1 Software for handling poultry health data base: Since the raw data collected from the various data generating centers (figure 10) had to be stored, retrieved and analyzed by using computers, a specific file handling software was developed for this project. The software used BASIC language and was designed in an interactive mode. It is simple and can be used to enter new data, and

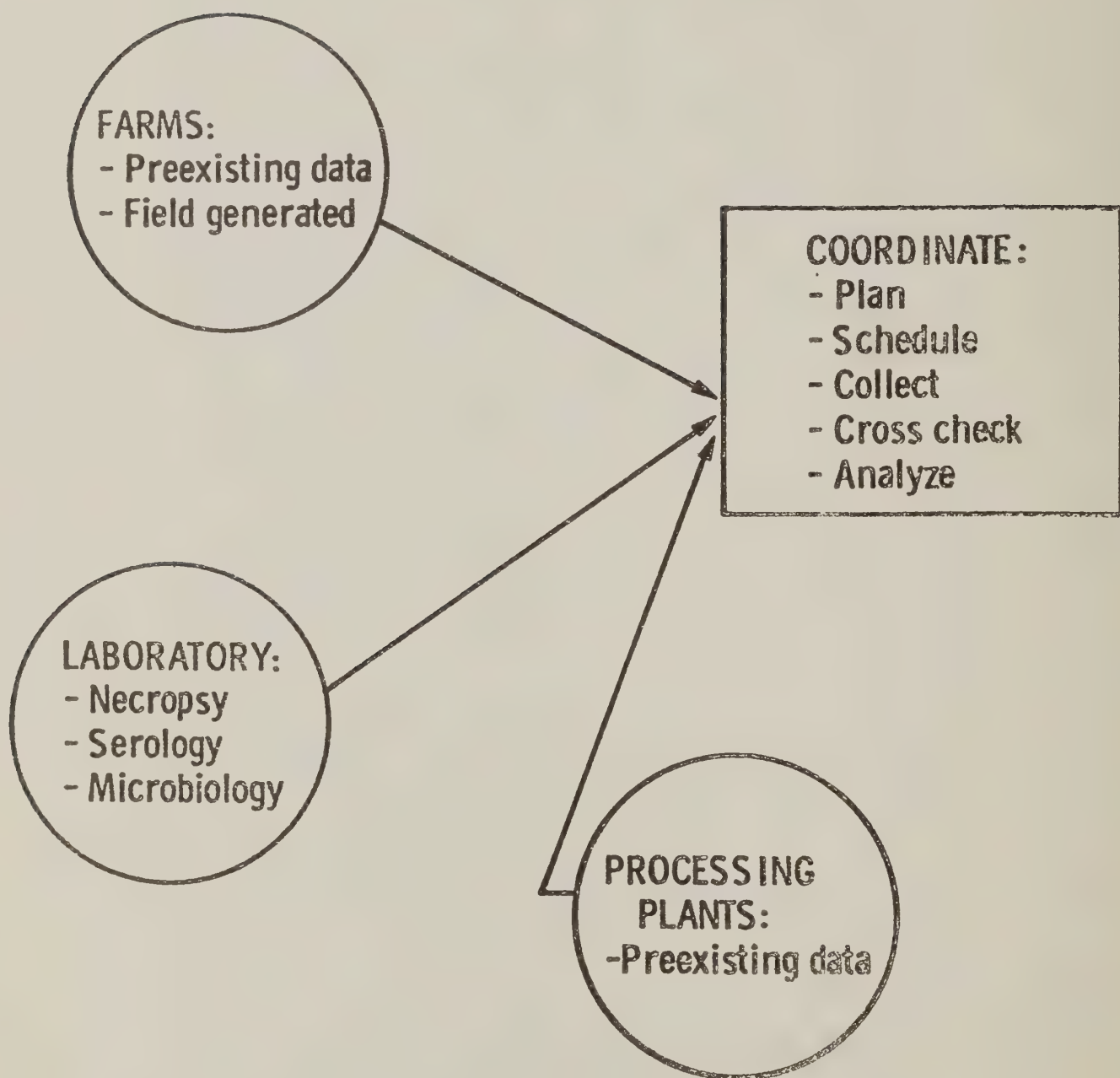


Figure 10 DATA GENERATING CENTERS

update or change existing ones in the data base. With a short introduction to its use, persons with little training will be able to apply it. The data were stored on floppy diskettes in a model II Radio Shack Microcomputer. There are three main data files which include:

- file for entering variable data for which no computation from tables were required.
- file for handling data to perform analysis, using the biomedical data program (BMDP) statistical package.
- file for storing confidential information on the firms and farms involved in this study.

To facilitate the analysis of data for descriptive and multivariate statistical methods using biomedical data program (BMDP package), FORTRAN files were created. In the early stages of the project since a large number of predictor variables ( $X_i$ ) were involved, the variables were partitioned into:

- hatch data
- broiler data
- biological and feed data,
- transit and processing data

Therefore, there were four sets of predictor variable groups, along with the respective condemnation rate data ( $Y_i$ ). Such groupings appeared to be satisfactory from the natural delineations that exist in the sequential events in poultry production, and the systems diagrams (figure

5-8) were useful in making such a decision.

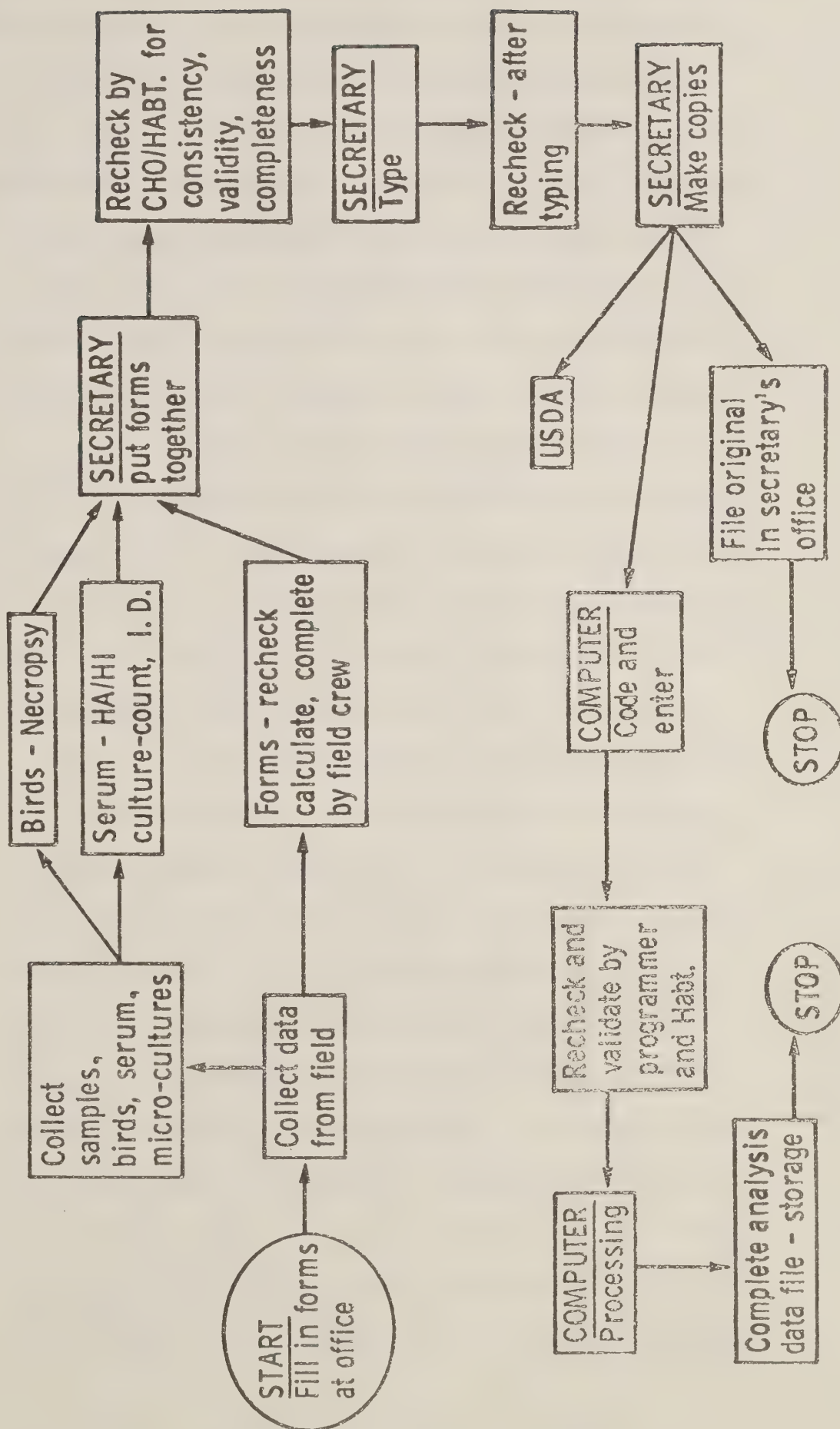
5.7.2 Validation procedures: The data generating centers for this study and the need for coordination of these data inputs were indicated in figure 11. In order to manage the incoming data, proper planning, scheduling, evaluation of data for validity and completeness was required. The steps involved and method of handling this aspect is described in figure 11. Note that the descriptive protocol for management of the study corresponded closely with the mechanism laid out for data handling in this figure. The incoming data were cross checked manually by the research associate and the principal investigators at least three times before it was finally stored in the computer data base.

It is significant to stress that careful data management is a crucial factor to the success of any project, and especially when a large volume of data is involved. Such as in this project, this point becomes even more critical. Thus, the data processing and management practices have been streamlined to ensure accuracy, validity and completeness throughout the life of the project.

5.8. Data analysis: With a background on the essence of the problem that we seek solutions for, a brief review of the literature pertaining to the systems concept and the use of multivariate models to develop the predictive equations in this task is also timely.



POULTRY LAB



#### 5.8.1 Review of the literature on data analysis: The systems

concept is a well tested problem solving scientific method which is widely accepted in engineering, economics, ecology, biological sciences, biometerology and human medicine (58-66). Although, it is relatively young in the area of veterinary medicine, it is now beginning to be applied to solving epidemiologic problems. Its future in veterinary medicine appears bright, and its application to examining the problem defined in this project could be one good example of such trends. The application of multivariate techniques to develop predictive or discriminative models is also widely used in various scientific and social disciplines where the background in the use of quantitative methods is well established. It is a standard statistical tool, the basis of which rests on sound mathematics (49, 67). In veterinary medicine, the application of multivariate techniques has been somewhat limited so far. In one such application, the best method for the control of African trypanosomiasis was investigated, and based on this result, rational disease control recommendations were obtained (68). Others have also used it to evaluate disease control methods (69, 70). In a recent study, discriminant analysis was utilized to classify a group of feed lot calves into poor or good doers (71). In the area of poultry health, the application of the systems concept and multivariate analytic models appears to be unavailable except for two

cases, both yet unpublished reports (72, 73). In those two reports, the relationship between various turkey production factors, condemnation and downgrading in turkeys were examined by using factor analysis. The data base for this study was obtained from the 1977 live bird production and processing data from one processing plant in California. Data from 48 flocks, representing 19 growers, were available for analysis. The results of that study indicated that "week of year placed", climate on day of processing and feed conversion may have some predictive value. Since the literature on the application of systems analysis and multivariate models in veterinary medicine and more specifically in poultry health is rather scanty, it is believed that the results of this project would add a little more to our present knowledge.

As mentioned earlier, relevant variables that affect the health of a population of birds at given sites and/or times, served as potential predictors for the prevalence of poultry diseases on farms, and the condemnation rate at slaughter plants. Data gathered for such a set of explanatory or predictor variables ( $X_i$ ) were examined for significant effects on the dependent variable ( $Y$ ) viz. condemnation rates at slaughter plants, by using the biomedical data program (BMDP) statistical package (57).

#### 5.8.2 Data Analysis Methods:

- 5.8.2.1 Descriptive Statistics: Detailed data descriptive statistics were conducted by using BMDP2D. This program

enables counting and listing of the distinct values for each variable in the analysis. It computes univariate statistics including the mean, median, standard deviation, skewness and kurtosis. It then plots the positions of several estimates of location on a line. From the histogram and other descriptive statistics, the type of distribution and variabilities present in the data were assessed. P2D was followed by a scatter (bivariate) plot, whereby each of the predictive variables ( $X_i$ ) were plotted against the dependent variable i.e. condemnation rate ( $Y_2$ ), by using the BMDP6D program. This program computes and prints equations of simple linear regression and indicates the intersections of the regression lines with the frame of the plot. From such a scatter diagram, it was possible to obtain information on linearity or on the type of transformation which may be needed to lead to linearity.

5.8.2.2 Comparative (analysis of variance-BMDP2V): This program performs an analysis of variance (or covariance) for a wide variety of fixed effects models. In this analysis, the levels for a factor were specified by grouping it in a manner that would allow each factor to be evaluated, reither individually (one way analysis of variance) or cross classified with another factor (two way analysis of variance). The dependent variable with which each of the factors were evaluated was  $Y_2$ , the condemnation rate at processing.



As an example, flock size  $X_3$  could be grouped into three levels: flock size of 20,000 or less, 20,000 to 40,000 and over 40,000. The other variable to be considered could be  $X_{109}$ , the disease rate at necropsy. Three levels may be established for  $X_{109}$  as 0.2 or less, 0.2 to 1.0 and greater than 1.0. An analysis of variance using BMDP2V could be conducted to test the hypothesis:

- a) test of equality of row means:
- b) test of equality of column means:
- c) test of no interaction:

In this study, for example, the hypothesis tested were:

There is no difference in the response variable for the three categories of flock size ( $X^3$ ) which were laid out across rows. There is no difference in the response variable for the three categories of disease rate ( $X^{109}$ ) which were across columns; and that there is no interaction between the row and column factors.

One should note that in creating 3 or 4 levels of  $X_3$  (flock size) to set it in an ANOVA format, what one does is really group data in summary form rather than examine the true spread of that variable by looking at its actual values in a more continuous setting in the form of groupings or levels. More importantly, the basic objective was to devise a predictive model; not to assess

differences between variables.

5.8.2.3 Multivariate linear model layout: As indicated in the research proposal, the major thrust of the analysis was based on linear multivariate models. It was proposed that:

$$Y = f(X),$$

and the linear multivariate model:

$$Y = \beta_0 + \beta_1 X_1 + \text{-----} + \beta_K X_K + \epsilon_K$$

Where,

$Y$  = condemnation rate at the processsing plant,

$X_1 \text{ -- } X_K$  = determinants of condemnation rate, variable data collected from farms.

$\beta_0 \text{ -- } \beta_K$  = coefficients to be estimated, which indicate the relative strength or importance of each variable ( $X_k$ ) in predicting  $Y$ .

$\epsilon_K$  = random error term - unexplained variability.

A diagrammatic view of the linear causal model which is an abridged and simplified form of figure 8, but one which is more straight forward to see, is given in figure 12. Note that figure 8 was a dynamic representation of the problem, while figure 12 was the summarized static (still picture) form of the same problem. The array of data layout for the flock testing project compatible with the diagrammatic view of figure 12 is presented in figure 13.

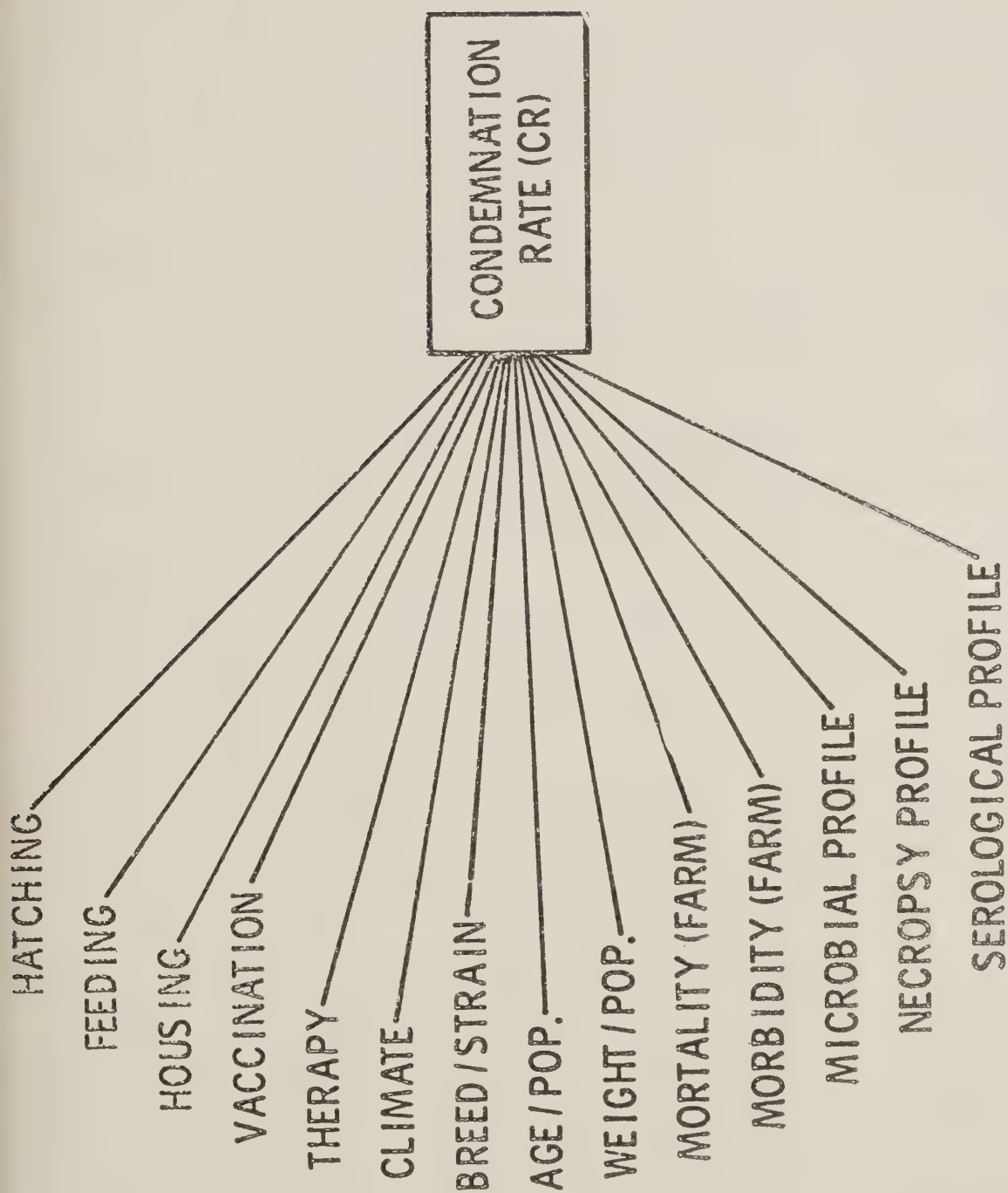


Figure 12

MULTIFACTORIAL CAUSAL MODEL LAYOUT FOR CONDEMNATION RATE (CR) OF POULTRY

Figure 13

The Data Base for a Multivariate Model  
Flock Testing Feasibility Study, 1981-82

Case No.	Y	$X_1$	$X_2$	$X_k$	
Brood 1	1	$Y_1$	$X_{1,1}$	$X_{2,1}$	$X_{k,1}$
	2	$Y_2$	$X_{1,2}$	$X_{2,2}$	$X_{k,2}$
	21	$Y_{21}$	$X_{1,21}$	$X_{2,21}$	$X_{k,21}$
Brood 2	22	$Y_{22}$	$X_{1,22}$	$X_{2,22}$	$X_{k,22}$
	49	$Y_{49}$	$X_{1,49}$	$X_{2,49}$	$X_{k,49}$
Brood 3	50	$Y_{50}$	$X_{1,50}$	$X_{2,50}$	$X_{k,50}$
	60	$Y_{60}$	$X_{1,60}$	$X_{2,60}$	$X_{k,60}$
Brood 4	61	$Y_{61}$	$X_{1,61}$	$X_{2,61}$	$X_{k,61}$
	96	$Y_{96}$	$X_{1,96}$	$X_{2,96}$	$X_{k,96}$
Brood 5	97	$Y_{97}$	$X_{1,97}$	$X_{2,97}$	$X_{k,97}$
	154	$Y_{154}$	$X_{1,154}$	$X_{2,154}$	$X_{k,154}$



The specific linear statistical models employed to develop the predictive model for condemnation rate were:

- a. Multiple linear regression - the objective was to establish a predictor equation for condemnation rate from a set of predictor variables. The assumptions in using multiple regression models, are standard as presented in regression texts (49, 50, 67)

Each of the assumptions were evaluated by performing residual analysis to see if any violations were made. Such a discussion would be found under the results and discussion section. For performing the regression analysis, the BMDPIR and BMDP2R programs were utilized. The BMDP2R was especially important since it is a stepwise procedure which facilitated the selection of the best subset of predictors for condemnation rates. This program (P2R) computes and estimates parameters of a multiple linear regression equation in a stepwise manner. Variables are allowed to enter into an equation (forward stepping) or are removed (backward stepping) from the equation, one at a time, according to any of four possible criteria to be selected. In this analysis, the F method was used, whereby the variable with the smallest F-to-remove was removed if its F-value was less than the preassigned value. If no variable meets this criterion, the variable with the largest F-to-enter was entered if

the F-to-enter exceeded the F-to-enter limit (57). Assuming that some of the predictor variables may require transformations e.g. logarithmic, such options were exercised as needed. P2R computes univariate statistics, covariance and correlation matrices, analysis of variance tables at each step, F-to-remove and F-to-enter values, and other information. A summary of variables entered, the multiple correlation coefficient (R) and the coefficient of determination ( $R^2$ ) were also provided along with residuals. A zero intercept equation useful for establishing the descriptive and comparative value of a variable, was provided. Since forward stepping was followed by backward stepwise regression, the potential predictive value of the variables were not lost.

Although the decision making criteria for variable elimination or selection from the data base will be discussed later, it is important to point out that the results from multiple regression would be evaluated by using F values, R and  $R^2$  levels to determine whether a selected variable(s) has biologically explainable correlation with poultry condemnation.

$R^2$  measures the proportionate reduction of total variation of the dependent variable ( $Y_2$ ) associated with the use of a set of independent ( $X_i$ ) variables. Generally, the higher the value of  $R^2$ , the better the usefulness of the model. Correspondingly, R measures the strength of correlation between the dependent and

independent variables. Both of these values are useful indicators of the predictive power of the model.

- b. Discriminant analysis is the other linear multivariate model used in this study. The objective in this case was to obtain a subset of discriminator variables which would enable one to classify a flock of birds from a given farm and/or house into high or low condemnation groups or more subgroups, based on predetermined criteria for such a decision.

To accomplish this, BMDP7M, a stepwise discriminant analysis procedure was employed. In this method, variables used in computing the linear classification functions were chosen in a stepwise manner with both forward and backward stepping options. At each step the variable that adds the most to the separation of the groups was entered into, or the variable that adds the least was removed from the discriminant function. A Jack Knife-validation procedure option was used to reduce bias in group classifications. In all statistical analysis to be performed, the level of significance was evaluated at either the 0.05 or 0.01 levels.

It should be reiterated that the main objective of this research was not to simply establish differences or associations but to develop a predictive model. Therefore, the two linear multivariate models presented above were selected as the most appropriate ones.

#### 5.8.5 Procedure for selecting the final predictor model(s):

After the total number of predictor variables have been reduced, the final aspects of data analysis to establish the predictive or discriminative models, was conducted in the following manner. Using an individual house on a farm as the experimental unit, cases for which a complete set of data were available for, were analyzed first. Secondly, using a farm as the experimental unit, comparable data analysis were performed. A decision as to whether to use the house or the farm as the experimental unit of choice was made based on detailed analysis of the data. Finally, to perform the validation of the model, the total number of cases were divided into two groups. The first set of cases formed the study data set. Based on these observations, the predictive/discriminative models were developed. The second group of cases served as the test data set. Once the multivariate models have been established, the validity or performance of the models were assessed using the cases from the test data set. In developing the predictive/discriminant models, BMDP2R and BMDP7M programs were used. For the discriminant model, various cut off points were used and the options discussed accordingly, including the probabilities and the consequences of misclassification. Results from the detailed descriptive statistics provided via PMDP2D and BMDP6D, and other statistical tests, specifically, analysis of variance were utilized where needed to reveal



5.8.6 Assessment of adequacy of model and validation: Once the predictive/discriminant models have been established, using study data, the validity of the models were evaluated by entering these data into the predictor equation and predicting the condemnation rate before inspection, and then comparing the prediction with the actual condemnation rate. A very important step at this stage was the assessment of the adequacy of the model by performing detailed residual analysis. A variety of computer generated residual plots were employed to identify the nature of lack of fit, outliers, deviation from normality and other deficiencies. This aspect of the analysis addressed the question of the basic assumptions involved in using linear models. Such assumption as linearity, homogeneity of variance and normality of distribution were evaluated. Where inadequacies existed, the variables of interest were transformed, for example to respective exponential or quadratic forms to improve the adequacy of fit. Correspondingly, confidence intervals were computed for the respective regression coefficients in the predictive model using Bonferroni's method (49). These techniques are all related to evaluate the validity of the predictive model and should provide useful information.

5.8.7 Weighted least squares: A weighted least squares procedure was used in the analysis of the data via BMDP2R.

Weighted least squares estimation is appropriate when the error variance is not homogeneous but varies from case to case. In the data base used in this analysis, the estimated standard deviations of the regression coefficients and the coefficient of variation of some variables indicated that weighted least squares could be useful to improve the predictor equation.

A two stage least squares procedure was used here as described below.

Weighted least squares: in BMDP2R weighted least squares procedure, the goal is for the estimates of the coefficients to minimize:

$$\sum W_i (Y_i - \hat{Y}_i)^2$$

Where  $W_i$  is the weight for case  $i$ . The problem though is in obtaining a value for  $W_i$  for each of the cases.

However, we know that:

$$\sigma^2(\epsilon_i) = \{E(Y_i)\} \{1 - E(Y_i)\}$$

and an appropriate weight estimate could be obtained by:

$$W_i = \frac{1}{\{E(Y_i)\} \{1 - E(Y_i)\}}$$

But,

$$E(Y_i) = \beta_0 + \beta_1 X_i$$

indicating that the above weighting procedure involved unknown parameters. One way to solve this problem was by using a two stage least squares procedure, i.e. in stage 1, using BMDP2R, stepwise forward and backward stepping, a regression model was obtained using a specific predictor

equation. In stage 2, estimates of the weights were obtained from the results in stage 1 above where:

$$W_i = \frac{1}{Y_{2i} (1 - Y_{2i})}$$

These estimated weights were then used to obtain the weighted least squares regression model. To enable this, a small Fortran subroutine was included to calculate  $W_i$  as given above and in the BMDP2R program, the variable which contained case weights was indicated appropriately. The adequacy of the model via weighted least squares and its residual analysis were performed as described earlier.

#### 5.8.8 Hardware and Software for Data Analysis (BMDP Package):

The analysis of the data collected was performed using BMDP statistical software on a VAX 11/750 computer at Tuskegee Institute. The sequence of statistical analysis consisted of:

BMDP2D - descriptive statistics for each variable;

BMDP6D - scatter plots of each predictor variable vs. the dependent variable;

BMDP2V - An analysis of variance program for specified factors;

BMDP1R - multiple regression program whereby all variables were entered for a specified dependent variable;

BMDP2R - a stepwise forward selection regression procedure followed by backward stepping. This enabled the evaluation of each predictor variable so as to

eventually select the best subset of predictor variables; and

BMDP7M - a stepwise discriminant analysis program to develop the classification function into high/low condemnation groups.

5.9 Decision making criteria for deleting variables from data base: From an understanding of the nature of the problem and based on a detailed causal analysis of variables which may influence condemnation rate of poultry (figure 8), 286 potential predictors (X's) were identified. This was a lengthy list of variables and systematic screening was needed to reduce the number of variables to a manageable level. The ultimate objective was to select only a very few, possibly less than 10 subset of predictor variables which could then be used for predictive or discriminative purposes. The reason for shortening the list of predictor variables was mainly because a multivariate model with a limited number of independent variables was easier to analyze and understand. But one has to be careful not to compromise predictive power. The search for the "best" set of independent variables is complex. The decision making criteria devised for this study were:

5.9.1 Phase I preliminary data screening variables deleted if:

- a. data on specific variables were missing and were unavailable,
- b. variable was redundant
- c. variable was not of fundamental importance to the



problem,

- d. computations of specific rates which enlarged the raw data for a variable e.g. disease specific/age specific mortality/morbidity rates. In some cases such specific rates were unavailable e.g. morbidity rates.

#### 5.9.2 Phase II second stage screening:

- a. Based on descriptive statistics, variables with large variability especially those with large coefficient of variation were considered for deletion.
- b. From scatter plot diagrams, variables were examined visually as well as by their simple linear regression results to see if transformations, such as logarithmic, quadratic forms or interactions could improve their linear form. If not, these variables, were considered as candidates for deletion.
- c. From a printout of correlation matrices of each group of variables, highly intercorrelated variables (high multicollinearity) were considered for reduction.
- d. After fitting a regression model containing an entire set of potential independent variables which may predict condemnations, those variables which had small absolute value of the t statistic were also considered candidates for screening.

At this stage, although any of the above criteria did not automatically lead to deletion of the variables, those that failed any two or more of the above criteria were

dropped from further consideration. It was believed that at the end of the second stage of screening, the final potential predictor variables could be narrowed down to between 30 to 50.

5.9.3 Phase III final stage of selection for the "best" set of independent variables for a predictive and/or discriminative model: The final screening of variables to arrive at the "best" set of predictor variables was basically accomplished by a computerized stepwise selection process which utilized forward and backward stepping techniques. The stepwise regression search method was widely used in many fields. In this procedure, the basic criterion for adding or deleting a predictor variable equivalently involved:

- reduction in sum of squares,
- partial correlation coefficient, or
- F statistic

Quite simply, at each step, the F statistic was computed by the computer program, and the predictor variable with highest F value was the candidate for addition. Conversely, in backward selection, the variable with the smallest F value was identified and if it was less than some predetermined limit, the predictor variable was dropped. More details on the involvement of such a selection process, specifically, when using BMDP2R and BMDP7M are available elsewhere (57). Once a set of predictor variables were identified, the final model was

examined further by performing a residual analysis to evaluate the adequacy of the model. A variety of residual plots were employed to identify the nature of lack of fit, outliers, deviation from normality and other deficiencies. The model building process did not stop at the conclusion of the selection of the "best" subset of predictor variables discussed above; until the final predictor equation was validated. This was accomplished by testing the predictor power of the model on a new set of data.

5.9.4 Strategy for data analysis: The first decision to be made in the data analysis task was to determine whether to use a house or the farm as the experimental unit. Data have been collected using both of these as study units and the analysis using two sets of data would have been cumbersome, expensive and time consuming. To settle this question, the following plan was devised. Initially to facilitate analysis, the data set were subdivided into 4 partitions or submatrices. This was necessitated since the number of variables in use at one time was large and beyond the limits of the BMDP package. However, during the last part of the project the BMDP package had already been expanded to handle up to 200 variables at the same time. Therefore, the partitioning of the matrices was not necessary in the final analysis of the data. On the other hand, for the decision of whether to use the house or farm as the study unit, the partitioned matrix approach was utilized since such an analysis was performed a few months

earlier. The partitioned matrices were labeled:

- a. Hatchery data—which contained data of hatchery related variables
- b. Broiler data—which contained variables related to broiler house environment
- c. Feed and biologicals data—which contained data pertaining to the use of feed and biologicals in poultry raising
- d. Transit and processing data—which contained variables dealing with the final phase of poultry production and processing

Such partitions appeared satisfactory from the delineations that are inherent in the sequenced events in poultry production. The systems diagram (Figure 8) was used for making such categorizations. By using the dependent variable ( $Y_2$ ) with each of the above partitioned matrices, the previously indicated sequence of BMDP programs were conducted. The goal was to reduce the number of variables from each of the respective matrices so as to end up with one final data base of about 30-50 predictor variables, thus compressing the 4 partitioned matrices into one data matrix for final analysis. After the decision of which experimental unit to use in the analysis was made, the final aspects of data analysis to develop the required models was initiated. The final data analysis were conducted after:

- a. Data for the last brood cycle (brood 5) was



entered on flock testing computer data base and all other information was updated, corrected and verified.

- b. The respective disease specific condemnation rates in addition to the condemnation rate due to all diseases ( $Y_2$ ) were entered into the data base. These were:  $Y_9$  (leucosis),  $Y_{10}$  (septicemia),  $Y_{11}$  (airsacculitis),  $Y_{12}$  (synovitis),  $Y_{13}$  (tumors),  $Y_{14}$  (others).
- c. The respective  $Y_{t-1}$  values (condemnation rate at one previous brood for each study farm) was entered along with the disease specific condemnation rates into the data base as one additional potential predictor variable.
- d. Data for  $X_{109}$ , the disease rate variables based on the necropsy profile performed at Tuskegee Institute, was entered along with the corresponding respective necropsy based disease specific rates for leucosis ( $X_{110}$ ), septicemia ( $X_{111}$ ), airsacculitis ( $X_{112}$ ), synovitis ( $X_{113}$ ), tumors ( $X_{114}$ ) and others ( $X_{115}$ ).

Once the decision of which study unit to use was made, all the predictor variables in the poultry data base were handled simultaneously in one sweep without resorting to partitioned matrices. This way, the influence of each variable in condemnation rate evaluated simultaneously along with all other potential predictor variables.

Therefore, a sequence of BMDP of analysis were performed with the specific objectives of:

- a. Developing a predictor/discriminator model for  $Y_2$  by using  $X_{109}$  as one of the many independent variables. Each of the disease specific condemnation rates ( $Y_9 - Y_{14}$ ) were handled in the same manner as  $Y_2$  but using their respective necropsy based disease rate variables ( $X_{110} - X_{115}$ ).
- b. Developing a predictor model for  $X_{109}$  itself as the dependent variable using the remaining independent variables. Each of the necropsy based disease specific rates were then evaluated individually by replacing  $X_{109}$  as the dependent variable.
- c. By replacing the value of  $X_{109}$  in the predictor/discriminator model for  $Y_2$  using the result of the prediction of  $X_{109}$  from section b, the predicted value for  $X_{109}$  was used in the model thus bypassing the need to perform necropsies before the birds were processed. However, one has to accept the level of error present when using the predictor model for  $X_{109}$  as an input to another predictor equation.

## 5.10 Limitations faced in the project

- ### 5.10.1 Research design related: A problem inherent in the research design itself was the lack of a random sampling

of study firms and farms to serve as the experimental unit. Because of this drawback, the inferences to be made from the results will have to be guarded. It is important to note that although such a sampling procedure was desirable from the statistical standpoint, it was neither practical nor feasible. From a total of 11 major poultry firms in Alabama, nine of them were requested to cooperate in the study and only three accepted to do so initially. Eventually two others joined the project. The firms studied were satisfactory in terms of the representations of the poultry firms in Alabama. On the other hand, the random samplings of growers would have been desirable; however, the question of cooperation and logistics were overriding factors in the decisions made in this study.

5.10.2 Field data collection related problems: Problems encountered in dealing with growers as well as those which arose in the processing plants are presented below, in summary form:

- a. Lack (or loss) or cooperation of study units.  
Some growers restricted the visits made by the research team, and data gathering was hampered.
- b. Unavailability of farm data-records on such variables as morbidity, medications, feed utilization and microclimatic data  
(temperature and humidity) were not available.

When requested to keep some of these records, most of the growers were unwilling to do so.

- c. Some of the study farms ceased to raise chickens, and data on these farms could not be followed up during the whole year.
- d. The logistics of gathering data from hatcheries, farms and processing plants was beyond the original contractual agreement of 2 farms per firm.

Originally, quite often, 2 or 3 teams were sent to the field at the same time performing microbial samplings of hatcheries and farms, collecting weekly feed utilization data, visiting each brood of broilers on different farms to collect blood samples and existing data, and collecting blood and necropsy samples from processing plants. This usually involved long hours of driving at night and day. Because of the exhaustive schedule as well as shortage of manpower, the number of study farms were later reduced to 3 or 4 per firm while still maintaining representation across the three strata of production performance rankings.

- e. Weekly feed utilization data remained elusive since such data were not kept by the poultry growers. An estimation procedure was developed to accomplish this phase of the study. Since the procedure involved rough estimations, the accuracy and usefulness of



such data was limited, it did however, provide some preliminary indication of patterns of feed utilization among farms. Due to the demand on time and manpower, the data collection of weekly feed utilization from study farms was conducted in the following manner:

- Data were collected from north Alabama study farms only if other tasks such as 4 or 7 week data collections or microsampling were performed, thus limiting the amount of travel to a manageable level. This also meant that feed utilization data was unavailable on regularly scheduled weekly visits.

- Data from study farms in south Alabama were collected on a weekly basis on week-ends since these farms were relatively close to Tuskegee Institute.

The possibility of developing a flow meter type of device which could automatically record the volume of feed being utilized on chart paper, on a daily basis was explored. Although the idea appeared feasible, it was not pursued further due to lack of time for development of such a device. This is an engineering problem,

and one has been intrigued why the industry has not already developed such a feed utilization monitoring device since feed cost is one of the major expenses that the grower has to contend with. Our discussion with a few growers on this subject and on the possibility of designing such a device confirmed the need and the demand for such an instrument.

- f. The collection of condemnation data by house was another problem area. One company declined to assist us in the collection of such data. Occasionally, even in other processing plants who have volunteered to keep track of slaughter birds on a house by house basis, flocks from two houses were mixed together during shipping of birds from the farms to slaughter plants. Although every effort was made by the research team to maintain the identity of lots on a house basis, the problem appeared to be ever present and because of that, some condemnation data on house basis were unobtainable.
- g. Unavailability of trim data due to diseases: condemnation due to diseases involved either whole carcass or parts trimmed. Records furnished by IIC of FSIS on whole carcass

condemnation were accurate. However, data for trimmings due to diseases was unavailable.

The processing plants kept all trimmed parts, regardless of causes for condemnation, in one container, i.e. trimmings due to diseases as well as those due to plant errors were all placed in one container and then weighed.

Diseased parts trimmed and condemned were for such categories as necrotic dermatitis, patchy skin disease, breast blisters, and slip tendons. Conversely, trimmed parts due to plant errors include such items as mangled birds, bruises, broken bones or skin, hemorrhage in legs, wings, thighs or backs, etc. All these condemned parts were placed together, since FSIS does not require processing plants to acquire and maintain records on trimmings.

Yet, a considerable amount of time and energy of the inspector on the line were actually devoted to identifying and indicating what parts were to be trimmed and how much. Trimmings due to diseases appear to contribute substantially to the condemnation rate of a flock. The keeping of such data should be standard practice by FSIS, since both in terms of disease surveillance, and inspection manpower requirements, the task of trimming would have to be considered emphatically. Additionally,

the expertise required in identifying trimmed parts due to such diseases as tendonitis, abdominal flap sore, patchy skin disease, hock deformation, breast blisters trims, etc. may not be standard from plant to plant. As the disease condemnation of whole carcass decreases, condemnation due to parts trimmed may become significant and yet as the system operates currently, such data are unavailable. Therefore, relevant comments on such trends could not be made.

#### 5.10.3 Laboratory related problems:

- a. Necropsy profile, (X109)-described in great detail earlier was an attempt to obtain an estimate of disease rate on a study farm from 200 randomly selected birds at processing plants for necropsy examination at Tuskegee. Since the purchase of birds was a rather costly one, data for this variable was somewhat limited.
- b. Microbial sampling: The need for an expanded microbial profiling work has been presented in our systems diagrams (Figure 8). The necessity for performing microbial population estimates by colony counting as well as the identification of the types of organisms in the hatchery and poultry house ecosystem has been described. The identification of microbial flora using semiautomated equipment to handle the large volume of samples in this project was essential. Unfortunately semiautomated microbial identification



equipment and supplies were not included in the original budget. Because of the strong conviction of the investigators on the need for this aspect of the study, a limited number of samples were identified by using manual procedures during brood cycles 4 and 5. The limited nature of this part of the study provided only descriptive information. The number of cases generated were not sufficient enough to be evaluated along with the other predictor variables. One cannot overemphasize the potential importance of microbial profile data in affecting condemnations (especially the types of organism which predominate the poultry ecosystem) since these are central in affecting the biodynamics of poultry health.

5.10.4 Data analysis related constraint: One of the crucial techniques for data analysis calls for the use of a discriminant analysis model. The objective was to devise a discriminating mathematical equation to separate condemnation rates into at least two groups. This was accomplished only if prior decisions are specified as to how to separate condemnation rates into high or low; high, medium or low categories. This meant specific numerical values or cut off points had to be established prior to analysis of the data. In the progress report of August 1981, FSIS was requested to provide such a differential criteria so that the discriminant classification functions could be developed. However, FSIS declined to provide

such guidelines since they did not have numbers on what constitutes "high" or "low" condemnation rates. It should be noted that even for the predictive models being developed, prior demarcation lines have to be established for condemnation rates in order to provide guidelines as to when to implement possible scaled down inspection procedures, as opposed to continuing the current practice of inspection. Therefore, in this study arbitrary cut off points based on the existing data base were utilized in the analysis. Since a practical decision making criteria was unknown, therefore, time was spent trying various options which could have been avoided otherwise.

## 6. RESULTS AND DISCUSSION

6.1 The data base: The research design whereby the determinants of poultry population health were systematically identified and scrutinized via causal diagrams and predictive multivariate epidemiologic models have been described earlier. It was also noted that poultry (broiler) production involves a sequentially determined set of events which include breeder flock sources, the hatching, brooding and growing ecosystem and variables which result from poultry processing efforts. All variables in these various sites were identified, and appropriate quantitative data were collected, forming the data base.

A tabular summary of the study subjects (firms, farms, and the individuals houses of cooperating farms) for the respective brood cycles is provided in table 5. The complete set of data on both the independent and dependent variables is in Appendix 4; the complete list of the variables for which adequate data was collected is in appendix 9. The data base contained a maximum of 154 cases for 141 variables. Of these only variables  $Y_2$ ,  $Y_9$ - $Y_{14}$ ,  $X_{109}$  and  $X_{110}$ - $X_{115}$ , served as the dependent variables, while those with subscript  $X_k$  (113 variable) formed the independent variables. The other Y subscripted variables  $Y_1$ ,  $Y_3$ - $Y_8$ , and  $Y_{15}$ - $Y_{17}$  were included for comparative purposes only. Although there were a maximum

TABLE 5 Study Units For Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

STUDY UNITS	BROODS					TOTAL # OF OBSERVATIONS
	1	2	3	4	5	
No. of Firms	3	4	5	5	5	22
No. of Farms	21	27	31	31	28	138
No. of Houses	45 (4)	58 (26)	67 (27)	68 (12)	50 (16)	299
No. of Houses with Condem- nation data	6	26	27	12	16	87
No. of Houses with Necropsy and Condemnation data	6	11	22	9	0	47
No. of Farms With Condem- nation data	21	27	31	31	28	138



of 154 cases, all cases did not contain the complete set of predictor variable data corresponding with each dependent variable. Therefore, the number of cases with a complete set of data varied, depending on which multivariate variable were used.

6.1.1 Preexisting data - a major facet of this study was the collection of data from existing records kept by a broiler farm, processing plant or hatchery. Such information was acquired at specific times and for specified variables (Appendix 1, 2). Selected examples of those which comprise part of the data base are given in tables 6 - 8. The first table provides a segment of the poultry population profile and significant paramets in the flock testing study. In table 7a, specific preexisting data for condemnation rates of chickens from the five study firms, which spanned a year of study, are presented. Table 7b presents related information on a disease specific basis; the specific disease being leucosis, septicemia, airsacculitis, synovitis, tumors, and others, as provided by FSIS inspectors operaing in the five study firms.

6.1.2 Field generated data - the data collected in this manner formed part of the flock testing study data file, a computer printout of which is in appendix 3. Of the field generated data, the one with special significance is feed utilization. It should be noted that a good portion of feed utilization data at 4 weeks and 7 weeks of age was available from the records of the firm or poultry farm.

TABLE 6: Population Profile - Flock Testing Feasibility Study,  
Tuskegee Institute 1981-82)

STUDY	UNIT	FLOCK SIZE AT	MORTALITY RATE (%)		CONDEMNATION RATE (%)
FIRM	FARM	Wk. #1	4 Wk.	7 Wk.	PROCESSING
A	A11	15401	2.944	3.426	0.649
	A21	15005	2.316	4.496	1.948
	A31	48897	1.613	2.146	1.01
	A41	60864	2.980	3.512	1.302
	A51	15501	3.347	3.725	0.631
	A61	20800	2.947	3.637	0.962
B	B11	31729	1.440	2.134	0.255
	B21	26442	3.604	4.006	0.138
	B31	14243	0.761	1.232	0.212
	B41	41648	2.694	2.060	0.204
	B51	30609	1.309	1.627	0.232
	B61	25373	4.021	4.672	0.146
	B71	66323	1.377	2.028	0.182
D	D11	48100	2.351	3.092	0.934
	D21	47847	2.612	3.167	0.714
	D31	43561	2.587	2.937	1.037
	D41	53403	1.894	2.857	0.658
	D51	30093	1.785	2.620	2.044
	D61	60355	2.200	2.833	0.896
	D71	25051	1.713	5.716	
E	E11	10669	8.420	9.609	0.551
	E21	17574	0.946	1.581	0.601
	E31	27241	2.177	2.984	0.780
	E41	34245	2.806	3.207	0.444
	E61	25862	4.301	5.728	1.892
	E71	42525	1.310	1.866	0.387
F	F11	9901	2.176	3.189	0.550
	F21	29569	2.733	3.324	0.368
	F31	29489	3.118	4.606	0.401
	F41	39243	3.005	5.991	0.263
	F51	11845	2.145	5.319	0.220
	F61	34476	3.326	6.814	0.382
A	A12	15017	3.378	0.038	0.648
	A22	15156	3.950	4.363	0.508
	A32	46729	3.636	4.774	0.542
	A42	61675	3.106	3.513	0.463

TABLE 6: Population Profile - Flock Testing Feasibility Study  
Tuskegee Institute (1981-82)

STUDY UNIT		FLOCK SIZE AT	MORTALITY RATE (%)		CONDEMNATION RATE (%)
FIRM	FARM	Wk. #1	4 Wk.	7 Wk.	PROCESSING
A	A52	15463	2.868	4.085	1.417
	A62	19958	3.553	4.814	0.450
	A72	33087	2.894	3.464	0.747
B	B12	26596	2.500	3.631	0.221
	B22	26843	1.649	2.277	
	B32	14091	1.348	2.497	0.543
	B42	41890	1.511	2.311	0.288
	B52	31297	3.178	4.090	0.259
	B62	27750	2.437	3.214	0.084
	B72	63818	1.481	1.813	0.249
D	D12	47877	2.239	2.870	0.662
	D22	47732	2.616	3.413	1.117
	D32	43754	2.486	3.894	2.703
	D42	53479	1.931	2.957	1.207
	D52	30304	1.024	1.587	0.401
	D62	60479	1.604	2.642	0.477
	D72	25025	1.319	3.110	0.816
E	E12	11215	2.068	2.727	0.686
	E22	15876	2.217	4.133	1.319
	E32	27181	2.487	3.549	0.940
	E42	34184	4.180	6.104	1.115
	E62	26474	3.225	2.123	1.209
	E72	39218	4.484	5.067	0.380
F	F12	10420	1.557	2.659	2.033
	F22	29557	2.669	3.965	0.472
	F32	29399	3.961	5.675	0.330
	F42	40825	2.926	3.865	0.412
	F52	11866	1.989	2.547	0.414
	F62	35368	3.521	5.708	0.321
A	A13	15563	1.994	2.374	0.720
	A23	15174	2.735	3.140	0.464
	A33	47366	3.497	4.371	0.433
	A43	60141	2.070	2.673	0.425
	A53	15311	1.396	2.544	0.280
	A63	20288	2.943	4.472	0.621
	A73	32129	1.743	2.606	0.460

TABLE 6: Population Profile - Flock Testing Feasibility Study,  
Tuskegee Institute (1981-28)

STUDY UNIT		FLOCK SIZE AT	MORTALITY RATE (%)		CONDENATION RATE (%)
FIRM	FARM	Wk. #1	4 Wk.		PROCESSING
B	B13	26368	1.219	1.931	
	B23	24,874	1.272	2.124	0.344
	B43	40339	0.849	1.761	0.137
	B53	29870	3.246	3.683	0.239
	B63	25192	1.566	2.380	0.226
D	D13	48173	1.480	2.180	5.800
	D23	47261	3.451	4.091	1.927
	D33	44178	1.499	M	1.023
	D43	53635	1.416	M	1.002
	D53	30209	1.642	M	0.865
	D63	64418	1.427	M	0.982
	D73	26823	1.635	2.475	0.947
E	E13	12265	3.666	4.311	0.314
	E23	19146	2.109	2.395	1.157
	E33	26595	6.450	9.646	
	E43	39099	3.269	4.821	0.296
	E63	30001	2.540	4.951	0.754
	E73	47184	3.017	4.901	0.790
F	F13	8495	3.018	4.287	
	F23	28918	4.738	5.839	0.282
	F33	29083	5.474	6.636	0.203
	F43	39243	3.117	3.713	0.205
	F53	11569	5.005	5.578	0.833
	F63	34281	3.660	4.585	0.595
A	A14	15356	2.669	4.242	0.938
	A24	15376	1.706	2.642	0.573
	A34	46344	2.313	2.953	0.377
	A44	73168	1.654	2.281	0.494
	A54	15278	2.744	3.623	0.529
	A64	20655	1.806	3.062	0.742
	A74	32046	1.932	3.044	0.700
B	B14	26817	1.477	2.219	0.367
	B24	24040	1.292	2.028	0.243
	B44	41743	1.288	2.299	
	B54	30219	1.626	2.205	0.248
	B64	27072	1.423	1.990	0.114



TABLE 6: Population Profile - Flock Testing Feasibility Study  
Tuskegee Institute (1981-82)

STUDY UNIT		FLOCK SIZE AT	MORTALITY RATE (%)		CONDEMNATION RATE (%)
FIRM	FARM	Wk. #1	4 Wk.	7 Wk.	PROCESSING
D	D14	48310	1.822	2.593	0.674
	D24	48255	1.980	2.829	0.579
	D34	43790	1.644	M	0.797
	D44	53155	1.813	2.876	0.618
	D64	64411	2.595	3.657	0.449
	D74	24774	2.417	M	0.868
E	E14	11352	1.378	2.463	0.214
	E24	17750	2.979	5.847	
	E34	30260	2.212	4.102	0.232
	E44	36276	3.692	4.928	0.423
	E64	27046	M	M	
A	A15	15504	2.167	2.816	0.747
	A25	16133	1.911	2.843	0.936
	A35	49193	1.715	2.379	0.691
	A45	68944	2.321	2.999	1.020
	A55	15320	3.092	3.991	0.603
	A65	20774	2.542	3.960	0.888
	A75	32262	1.875	2.442	0.701
B	B15	26913	1.826	2.572	0.368
	B25	22266	3.257	4.109	0.365
	B45	42324	2.407	3.015	0.312
	B55	31862	1.503	2.154	0.559
	B65	25222	2.027	2.667	0.218
D	D15	47463	3.435	4.729	0.677
	D25	47982	1.937	2.860	0.730
	D35	42910	1.941	2.622	0.617
	D45	53285	1.911	2.929	1.222
	D55	29183	2.860	3.229	0.478
	D65	64375	1.722	2.396	0.905

Table 7a: Condemnation Rate Due to Diseases for Study Farms

Firm	Brood				
	1	2	3	4	5
A	0.649	0.648	0.720	0.938	0.747
	1.948	0.508	0.464	0.573	0.936
	1.010	0.542	0.433	0.377	0.691
	1.302	0.463	0.425	0.494	1.020
	0.631	1.417	0.280	0.529	0.603
	0.962	0.450	0.621	0.742	0.888
	0.672	0.747	0.460	0.700	0.701
B	0.255	0.221	0.231	0.367	0.368
	0.138	0.171	0.344	0.243	0.365
	0.212	0.543	-	-	-
	0.204	0.288	0.137	0.211	0.312
	0.232	0.259	0.239	0.248	0.559
	0.146	0.084	0.226	0.114	0.218
	0.182	0.282	-	-	-
D	0.934	0.662	5.800	0.674	0.697
	0.714	1.177	0.902	0.579	0.730
	1.037	2.703	1.023	0.797	0.617
	0.658	1.207	1.002	0.618	1.222
	2.044	0.401	0.865	0.331	0.478
	0.896	0.477	0.982	0.449	0.905
	0.488	0.817	0.960	0.868	-
E		0.551	0.686	0.314	0.214
		0.601	1.319	1.477	0.326
		0.780	0.940	1.734	0.232
		0.444	1.115	0.296	0.423
		-	-	-	-
		1.892	1.209	0.754	-
		0.387	0.380	0.790	-
F			0.550	2.033	0.470
			0.368	0.324	0.283
			0.401	0.330	-
			0.263	0.412	0.295
			0.220	0.414	0.836
			0.382	0.321	0.598
			-	-	-

Table 7b:

Condemnation Rates and Disease Specific Rates by Study Firms for 5 Brood Cycles  
(1981/82)

	Y2	Y9	Y10	Y11	Y12	Y13	Y14
Firm 1 Brood 1	1.025	0.111	0.423	0.223	0.072	0.072	0.179
Firm 2 Brood 1	0.196	0.002	0.173	0.005	0.006	0.009	0.0
Firm 3 Brood 1	0.967	0.029	0.270	0.510	0.046	0.074	0.038
Firm 4 Brood 1	0.776	0.007	0.645	0.175	0.0	0.0	0.0
Firm 5 Brood 1	0.364	0.008	0.262	0.071	0.009	0.021	0.0
Firm 1 Brood 2	0.682	0.005	0.326	0.118	0.005	0.025	0.203
Firm 2 Brood 2	0.264	0.002	0.202	0.01	0.0	0.010	0.013
Firm 3 Brood 2	1.063	0.005	0.250	0.704	0.032	0.044	0.028
Firm 4 Brood 2	0.942	0.010	0.695	0.134	0.001	0.019	0.077
Firm 5 Brood 2	0.639	0.003	0.509	0.091	0.004	0.033	0.0
Firm 1 Brood 3	0.486	0.006	0.276	0.060	0.007	0.031	0.105
Firm 2 Brood 3	0.235	0.005	0.217	0.008	0.002	0.002	0.0
Firm 3 Brood 3	1.648	0.012	0.336	1.177	0.032	0.042	0.049
Firm 4 Brood 3	0.894	0.009	0.635	0.087	0.003	0.024	0.124
Firm 5 Brood 3	0.496	0.005	0.339	0.094	0.003	0.061	0.0
Firm 1 Brood 4	0.622	0.004	0.375	0.109	0.003	0.033	0.091
Firm 2 Brood 4	0.237	0.002	0.211	0.014	0.005	0.007	0.0
Firm 3 Brood 4	0.617	0.005	0.316	0.225	0.014	0.041	0.028
Firm 4 Brood 4	0.299	0.006	0.185	0.05	0.003	0.046	0.009
Firm 1 Brood 5	0.798	0.017	0.440	0.148	0.003	0.088	0.103
Firm 2 Brood 5	0.364	0.012	0.317	0.022	0.001	0.012	0.0
Firm 3 Brood 5	0.775	0.017	0.263	0.377	0.017	0.089	0.094

However, the one of interest from the standpoint of population health characterization, was weekly feed utilization rate. As described under methodology, this task was rather difficult and expensive and only a limited amount of information was available for it. An example of one such data is presented in figure 14. Since the number of study farms for which such data could be collected were few, the feed utilization on a weekly basis has not been in the analysis. Other variables for which field measurements or evaluations were conducted included weight of birds at 4 and 7 weeks, ( $X_2$ ), and proportion of undersized birds ( $X_7$ ). In such cases, 50-100 birds were selected arbitrarily and the necessary procedures performed to generate the data of interest.

6.1.3 Laboratory generated data - three specific types of laboratory related profiles are considered here.

a. Microbial profiling - two aspects were involved.

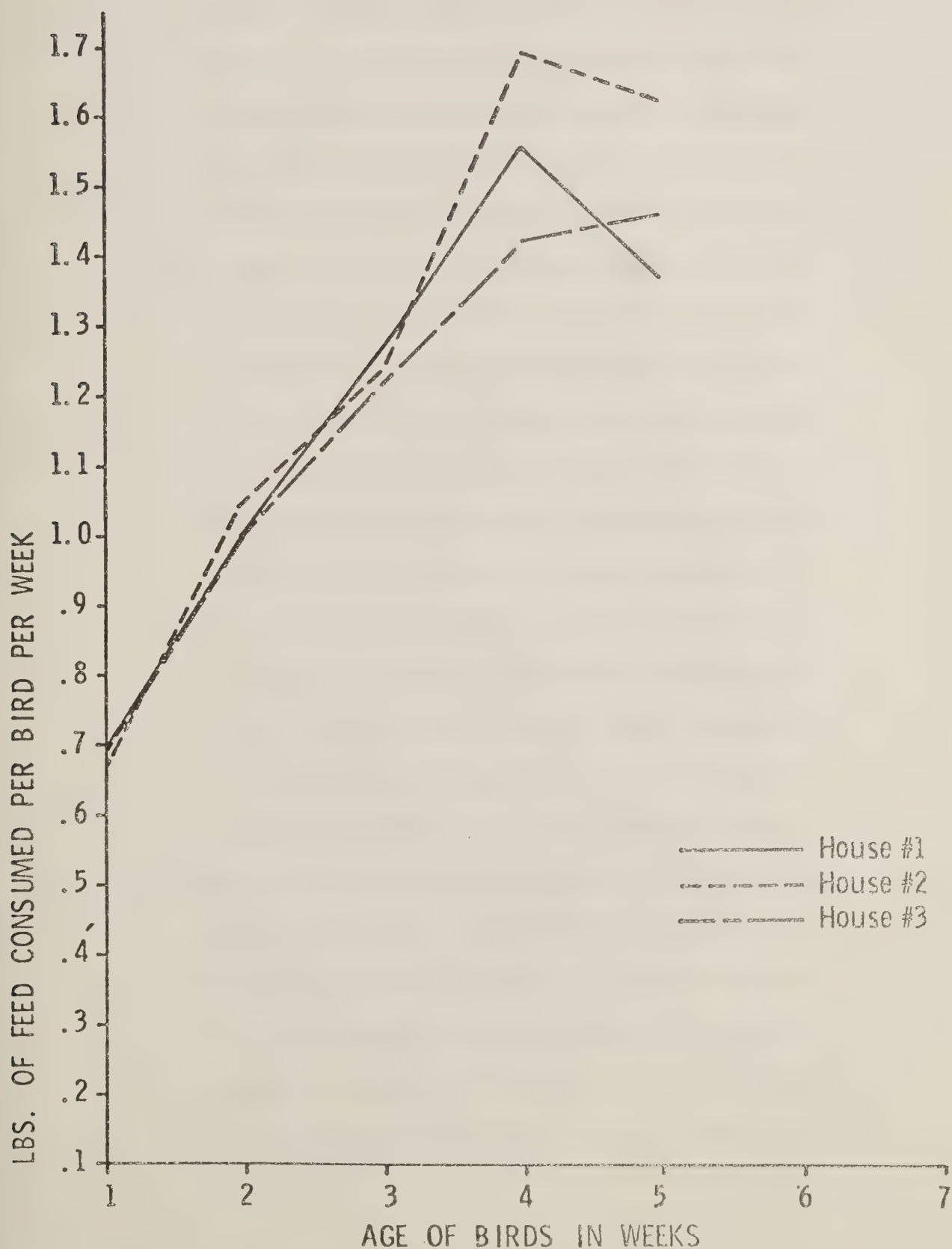
Firstly, the quantitative estimation of the microbial population size in hatcheries and in the poultry houses as described earlier. Secondly, the isolation and identification of the types of microorganisms which predominate in the broiler house and hatchery environment. The results of this work are provided in Appendix 5.

The limited studies on microbial profile in hatcheries and broiler farms did not offer clear indicators of whether bacterial and fungal populations in hatcheries and chicken houses



Figure 14 WEEKLY FEED UTILIZATION OF BROILER BIRDS  
IN SELECTED FARMS (example 3)

Flock Testing Feasibility Study, Tuskegee Institute (1981/82)



would directly relate to condemnation. There were few bacterial and fungal colonies isolated from the hatcheries, however, the bacterial and fungal populations in broiler houses were much larger. Non-pathogenic or low pathogenic bacteria do not pose serious health problems for poultry flocks. However, the pathogenic ones cause diseases of significance to the poultry industry. Therefore, the identification and characterization of the bacteria isolated from these study farms were required. Colonies from twenty-six cases were studied, the data of this study is summarized in Appendix 5. Most bacteria isolated from the hatcheries and broiler houses were non-pathogenic, however, several potential pathogens (bacteria and fungi) were also isolated. These were *Staphylococcus*, *Moraxella* spp., *Pasteurella*, *Pseudomonas*, *Proteus*, *Listeria*, *Corynebacterium*, *E. coli*, *Klebsiella*, *Streptococcus*, *Aspergillus*, *Rhizopus*, *Mucor*, and *Penicillium*. One of the potential causes of airsacculitis, *Aspergillus* spp. were isolated from 11 cases out of 26 studied. The result of this study indicated that there numerous potentially pathogenic organisms in the hatcheries and broiler houses examined during 1981-82. These organisms may cause serious health problems

under favorable environment. Therefore to monitor bacterial and fungal population in poultry houses and hatcheries may be necessary for a well managed poultry enterprise. Due to the limited nature of the data studied in comparison to the rest of the multivariate data collected during the life of the project, the data obtained from the microbial profile were not analyzed with the rest of the data.

- b. Serology profile - the result of this work is provided in Appendix 6, for the test sera which were collected from birds at 4 weeks of age. The titers for Mycoplasma synoviae were negative except for 5 study farms. These had a titer of 1.:10. In the case of Mycoplasma gallisepticum, only one study farm had a titer of 1:10, the rest were all negative. The titers for Newcastle disease varied from 1:10 to 1:80. Only three farms had a higher titer of 1:80, 10 farms had a titer of 1:40, 15 farms had a titer of 1:20 and 20 farms had a titer of 1:10. In Newcastle disease, most of these are vaccination related titers. The question was what level of titer could be used as the best predictor of the condemnation rate ( $Y_2$ ). For such a decision, the Newcastle data was analyzed using P2R. However, none of the titers showed a good correlation with  $Y_2$ . Because of

this, the cut off for a positive titer useful for predictive purposes could not be determined. Therefore, the serology profile data provided only descriptive information and was not used with the rest of the multivariate data. The hemagglutination inhibition test for the sera collected from birds at the time of processing was conducted only for Mycoplasma gallisepticum. As in the case of the 4 week-serology, the few samples analyzed had negative titers. Additionally, due to the fact that information generated from sampling of birds at the time of processing was determined to be of limited practical value, it was felt that the serology data at processing was not critical. Therefore, it was not carried out in full.

- c. Necropsy profile ( $X_{109}$ )- in an attempt to obtain an estimate of the disease rate on the study farms, 200 randomly selected birds, at the time of slaughter, were necropsied and examined for the presence of gross pathological changes. The disease and the respective disease rates are provided in Appendices 7 and 8. The conditions considered were septicemia-toxemia, airsacculitis, synovitis, salpingitis, squamous cell carcinoma and necrotic dermatitis. The latter condition, was significant in terms of trimmings for



disease parts, which was unavailable from the processing plants. Therefore, the necrotic dermatitis rate could be indicative of the importance of trimmed parts in poultry condemnations. For comparative purposes, the disease rate, lesions, regardless of degree of seriousness which may result in whole bird condemnation as well as trimming of parts) based on necropsy ( $X_{109}$ ) and the condemnation rate reported by FSIS inspectors ( $Y_2$ ), were also provided. The rate for  $X_{109}$  varied from 0.114% to 5.8%

#### 6.2 Data analysis to determine the study unit of choice:

The first major decision to be resolved involved the question of which experimental unit to use for the lengthy series of data analysis. This was crucial from the standpoint of saving time and expenses in computing, as well as to simplify the complexity involved in performing analysis on two sets of data - one on a house basis and the other on a farm basis. Since comparable data, both on a house and farm basis, were collected only up to the end of the 4th brood cycle, this data base was used to resolve the question of which study unit (house or farm) to use in the final model development. The complete set of data on a house or farm basis are given in Appendix 4. Basic descriptive statistics of these are also provided in Appendix 4.

6.2.1 Variable Reduction: Based on detailed causal analysis of variables which may influence condemnation rate of poultry ( $Y_2$ ), systematic screening was needed to reduce the potential predictor variables to a more manageable level, of about 30-40 predictor variables.

The variable reduction decision criteria have been presented earlier under the research design methodology. Following those guidelines, the variable reduction steps were divided into 3 phases.

6.2.1.1 Phase 1 - preliminary data screening-using the criteria for selection as described under methodology; a large portion of the variables were screened out.

The variables selected at the end of phase 1 were:

X57, X58, X59, X53, X54, X60, X61, X62-X72, X74-X83, X84, and X100 for hatchery data;

X3, X221, X5, X222, X7-X10, X14-X28, X30-X33, X39, X40, X85-X91, X93, X94, X97, X98, X102, and X109 for broiler data;

X116-X125, X127-135, X138-X148, X164, X165, X169-X174, X177, X181, X182, X186, X189, X190, X192, X194, X202-X209, and X212 for feed and biologicals data; and

X223, X224, X226-X231, X235, X237-X240, X241, X243-X255 for transit and processing data.

6.2.1.2 Phase 2 - second stage variable-there were 159 potential predictor variables at the beginning of phase 2. Since the experimental unit was an individual house, as well as the farm, only one of the data base was used to proceed through the steps of variable reduction. As it is, a large number of computations were involved and performing the analysis, both on a house and farm basis, was unnecessary and

expensive. The larger data base with more cases and a more complete set of information was the farm data and therefore, it was used to conduct the variable reduction process.

To facilitate further data analysis, the data set were divided into 4 partitions or submatrices. These partitioned matrices were labelled:

Hatchery data which contained 34 predictor variables,  
 Broiler data which contained 42 predictor variables,  
 Feed and biological data with 56 predictor variables,  
 and Processing data with 27 predictor variables.

By using the respective  $Y_2$  value with each of the above partitioned matrices, the previously indicated sequence of BMDP programs which included BMDP2D, 6D, 1R and 2R were run and are reported below in the form of steps.

Step 1: The final set of variables which were selected from the 4 partitions, combined into one data base to facilitate the final stages or predictor model development are given in table 8. Note that in table 8, some variables had to be included in the final data base simply because these were needed to make the retention of other variables meaningful. For example, house type 2 ( $X_{17}$ ) was selected based on selection criteria however, in order to retain  $X_{17}$  in the final data base,  $X_{16}$ , house type 1 also had to be included, i.e. since  $X_{17}$  was an indicator variable, it can only be used meaningfully if the associated indicator variables  $X_{16}$  was also included. Such was the case for hatchery source variables, house type 1, air intake direction, exhaust direction, feed source, and vaccine source. At the end of step 2, the number of predictor variables were reduced to 45.

Table 8

Variables Selected at End of Step 1  
Flock Testing Feasibility Study, 1981-82

<u>Variable Code</u>	<u>Variable Name</u>	<u>Reason For Inclusion</u> <sup>a,b</sup>
X <sub>57</sub>	Hatchery Source 1	b
X <sub>58</sub>	Hatchery Source 2	b
X <sub>59</sub>	Hatchery Source 3	a
X <sub>51</sub>	Hatchery Source 4	a
X <sub>52</sub>	Hatchery Source 5	b
X <sub>53</sub>	Hatchery Source 6	a
X <sub>54</sub>	Hatchery Source 7	b
X <sub>62</sub>	Fertility Rate	a
X <sub>63</sub>	Hatchability Rate (Hatchery)	a
X <sub>65</sub>	Hatchability Rate (Brood)	a
X <sub>222</sub>	Slaughter Weight	a
X <sub>8</sub>	Strain Type 1	a
X <sub>9</sub>	Strain Type 2	a
X <sub>10</sub>	Strain Type 3	a
X <sub>16</sub>	House Type 1	b
X <sub>17</sub>	House Type 2	a
X <sub>18</sub>	Population Density	a
X <sub>19</sub>	Distance Between Houses	a
X <sub>45</sub>	Air Intake (Roof)	b
X <sub>23</sub>	Air Intake ENE	a
X <sub>24</sub>	Air Intake NNW	b
X <sub>25</sub>	Air Intake WSW	a
X <sub>46</sub>	Exhaust (Roof)	a
X <sub>26</sub>	Exhaust ENE	b
X <sub>27</sub>	Exhaust NNW	a
X <sub>28</sub>	Exhaust WSW	a
X <sub>39</sub>	Mortality Rate at 4 weeks	a
X <sub>40</sub>	Mortality Rate at 4-7 weeks	a
X <sub>85</sub>	Date of Placing	a
X <sub>87</sub>	Length of Time for Preheating	a
X <sub>221</sub>	No. of Birds Shipped	a
X <sub>14</sub>	No. of Strains on Farm	a
X <sub>122</sub>	Feed Source 1	b
X <sub>123</sub>	Feed Source 2	a
X <sub>124</sub>	Feed Source 3	b
X <sub>41</sub>	Feed Source 4	a
X <sub>169</sub>	Vaccine Source 1	b
X <sub>170</sub>	Vaccine Source 2	a
X <sub>171</sub>	Vaccine Source 3	a
X <sub>186</sub>	Sanitation Index	a
X <sub>189</sub>	Litter Type 1	a
X <sub>265</sub>	Litter Type 2	a
X <sub>235</sub>	No. Dead on Arrival	a
X <sub>241</sub>	No. of Inspectors	a
X <sub>224</sub>	No. of Hours Driving	a

\* <sup>a</sup> variable included because it fulfilled selection criteria

\* <sup>b</sup> variable included to make selected variable under (a) meaningful,



Step 2: Subsequently, using the farm data, with the 45 predictor variables, BMDP1R and BMDP2R programs were run. This time the selection criteria for retention were:

- if selected by forward stepping BMDP2R computer program
- if the correlation coefficient of the predictor variable vs. Y2 was  $> 0.1$  or  $< -0.1$
- if the absolute numerical value of the "t" statistic pertaining to the predictor variable was  $> 1.25$

The satisfaction of any one of these criteria allowed the predictor variable to be retained for the subsequent steps. Those variables selected are shown in table 9. At this stage only, 30 variables remained. Four predictor variables were deleted for the following reasons:

X45 = air intake direction via roof - there was only one case with such a value and so the variable was omitted.

X123, X124 = feed sources 2 and 3 actually represent the poultry firms themselves. Since the values for these variables were too broad and many factors affect the performance of the company and also since the result could not be generalized to other areas, these variables were dropped.

Table 9

Variables Selected At End of Step 2  
Flock Testing Feasibility Study, 1981-82

Var. Code	Var. Name	Selection by P2R	Correl. Coeff.	t value
X <sub>58</sub>	Hatchery Source 2	yes		
X <sub>52</sub>	Hatchery Source 5	yes		-1.29
X <sub>62</sub>	Average fert. rate	yes	0.2458	-1.489
X <sub>221</sub>	No. Birds Shipped	yes		
X <sub>9</sub>	Strain Group 2	yes		-2.445
X <sub>16</sub>	House Type 1	yes		-1.552
X <sub>17</sub>	House Type 2	yes		
X <sub>45</sub>	Air intake-roof	yes		
X <sub>24</sub>	Air intake-NNW	yes		
X <sub>26</sub>	Air exhaust ENE	yes		
X <sub>27</sub>	Air exhaust NNW	yes	0.3334	2.137
X <sub>85</sub>	Date of placing	yes		
X <sub>123</sub>	Feed Source 2	yes	0.3650	
X <sub>124</sub>	Feed Source 3	yes	0.3658	1.640
X <sub>171</sub>	Vaccine Manuf. 3	yes	0.1124	
X <sub>241</sub>	No. of Inspectors	yes	0.360	
X <sub>59</sub>	Hatchery Source 3	no	-0.3301	
X <sub>51</sub>	Hatchery Source 4	no	-0.1965	
X <sub>53</sub>	Hatchery Source 6	no	0.3433	
X <sub>63</sub>	Hatchability Rate	no	0.1565	
X <sub>65</sub>	Hatchability Rate (brood)	no	-0.2485	
X <sub>14</sub>	No. of Strains	no	0.2490	
X <sub>28</sub>	Exhaust WSW	no	0.2480	
X <sub>40</sub>	Mort. rate at 7 weeks	no	0.1233	1.570
X <sub>87</sub>	Length of Preheating	no	-0.1570	
X <sub>170</sub>	Vaccine Manuf. 2	no	-0.2225	
X <sub>224</sub>	No. of hrs. driving	no	-0.3615	
X <sub>235</sub>	No. dead on arrival	no	-0.1202	
X <sub>39</sub>	Mort. at 4 weeks	no		-1.391
X <sub>186</sub>	Farm Sanitation Index	no		-1.415

X186 = farm sanitation index was deleted because  
it was based on partially subjective  
criteria.

Thus, at the end of step 2 of phase II, 26 predictor  
variables were retained to be used in the final  
analysis to determine which experimental unit to use.  
At this point, the disease rate based on necropsy  
(X<sub>109</sub>) was added to the data base.

Step 3. The final 27 potential predictor variables

established at the end of Step 2 were further scrutinized and the following steps were taken.

Although hatchery sources No. 5 ( $X_{52}$ ) and No. 6 ( $X_{53}$ ) were useful predictors of condemnation rates in the study area since these sources could not be generalized to other areas, the indicator variables for hatchery sources were deleted. Similarly, the indicator variables for air intake and exhaust directions ( $X_{26}$ ,  $X_{27}$ ,  $X_{28}$ ) were also omitted. Thus only 18 predictor variables were retained. From an examination of the residual plots in steps 1 and 2, two outliers were identified and those 2 cases were removed. Outliers are extreme observations whose points lie beyond the scatter of the remaining residuals usually four or more standard deviations from zero. At this point though, two cases with outliers which showed standard deviations values of only 2 or 3 were removed from the data base to see if a better fitting model could be devised. For the final decision making process using the 18 selected predictor variables, BMDP2R was run both for the farm and house data.

6.2.2 Equations for determining the study unit of choice:

Case 1 - Study Unit = Farm

The preferred predictive model was obtained at the

end of Step No. 12 at the termination of the forward stepping procedure, the predictor model being:

$$\begin{aligned}\hat{Y}_2 = & -2.753 + 0.038X_{62} + 0.009X_{14} - 0.256X_{39} + 0.157X_{40} \\ & - 0.003X_{85} - 0.011X_{87} + 0.052X_{109} - 0.275X_{171} - 0.125X_{224} \\ & - 0.001X_{235} + 0.095X_{241} \quad (a)\end{aligned}$$

$$F \text{ Value} = 7.44$$

$$R = 0.8652 \quad n = 43$$

$$R^2 = 0.7485 \quad X_k = 19$$

$$\hat{Y}_2 = \text{predicted condemnation rate}$$

$$X_{62} = \text{avg. fertility rate}$$

$$X_{14} = \text{number of strains on the farm}$$

$$X_{39} = \text{age specific mortality rate at 4 weeks}$$

$$X_{40} = \text{age specific mortality rate at 7 weeks}$$

$$X_{85} = \text{date of placing of birds in brooder house}$$

$$X_{87} = \text{length of preheating of brooder house}$$

$$X_{109} = \text{disease rate based on necropsy}$$

$$X_{171} = \text{vaccine manufacturer No. 3}$$

$$X_{224} = \text{number of hours driving from farm to plant}$$

$$X_{235} = \text{number of birds dead on arrival}$$

$$X_{241} = \text{number of inspectors in plant}$$

$$n = \text{number of cases}$$

$$X_k = \text{number of predictor variables to select from}$$

$$R = \text{multiple correlation coefficient}$$

$$R^2 = \text{multiple coefficient of determination}$$

The predictive value in equation (a) was high and 74.85% of the total variability was explained by the model. Of course the predictive variables ( $X_k$ ) are indicated in the



equation.

Case 2 - Study Unit = house

The predictor model was:

$$\hat{Y}_2 = 0.0223 + 0.281X_{39} - 0.081X_{40} + 0.152X_{109} - 0.003X_{235}$$

$$R = 0.8365 \quad n = 29$$

$$R^2 = 0.6998 \quad X_k = 18 \quad (b)$$

Where:

$\hat{Y}_2$  = predicted condemnation rate

$X_{39}$  = age specific mortality rate at 4 weeks

$X_{40}$  = age specific mortality rate at 7 weeks

$X_{109}$  = disease rate based on necropsy

$X_{235}$  = number of birds dead on arrival at plant

$n$  = number of cases

$X_k$  = number of predictor variables to select from

The respective  $R$  and  $R^2$  values were 0.8365 and 0.6998. In this case, 69.98% of the variability was explained by this predictor model.

Case 3 - Study Unit = farm (via weighted least squares):

In this third case, a weighted least squares procedure was used in the analysis of the data via BMDP2R as presented under research methodology. Weighted least squares is a two stage procedure whereby in stage 1, using a predictor equation as obtained (e.g. equation a) and from this equation, estimates of the weights were obtained. The weighted least squares predictor model was:

$$\hat{Y}_2 = -0.264 + 0.027 X_{63} - 0.015 X_{65} - 0.142 X_{14} - 0.267 X_{16}$$

$$\begin{aligned}
 & -0.052 X_{39} + 0.001 X_{85} + 0.136 X_{170} - 0.096 X_{224} + \\
 & 0.051 X_{241} \quad (c) \\
 & (R = 0.8935, R^2 = 0.7983)
 \end{aligned}$$

where:

- $\hat{Y}_2$  = predicted condemnation rate  
 $X_{63}$  = average hatchability rates (%) for hatchery  
 $X_{65}$  = average hatchability rate (%) for brood  
 $X_{14}$  = number of strains on farm  
 $X_{16}$  = house type 1  
 $X_{39}$  = age specific mortality rate at 4 weeks  
 $X_{85}$  = age specific mortality rate at 7 weeks  
 $X_{170}$  = vaccine manufacturer no. 2  
 $X_{224}$  = number of hours driving from farm to plant  
 $X_{241}$  = number of inspectors in plant  
 $R$  = multiple correlation coefficient  
 $R^2$  = multiple coefficient of determination

Case 4 - Study Unit = house (via weighted least squares)

The weighted least squares procedure via BMDP2R for the case where the house was the experimental unit was handled in the same manner as described for the farm case. The result of the weighted least squares was:

$$\begin{aligned}
 \hat{Y}_2 = & 17.202 - 0.067 X_{62} - 0.052 X_{63} - 0.079 X_{65} + 0.184 X_{17} \\
 & - 0.123 X_{39} + 0.003 X_{85} + 0.053 X_{87} \quad (d) \\
 & (R = 0.8712, R^2 = 0.7590)
 \end{aligned}$$

where:

- $\hat{Y}_2$  = predicted condemnation rate  
 $X_{62}$  = average fertility rate (%) for hatchery

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{65}$  = average hatchability rate (%) for brood

$X_{17}$  = house type 2

$X_{39}$  = age specific mortality rate at 4 weeks

$X_{85}$  = date of placing of chicks in brooder house

$X_{87}$  = length of time for preheating (hrs)

$R$  = multiple correlation coefficient

$R^2$  = multiple coefficient of determination

The significant point to be made now when examining these four final equations is that it is to be remembered that there was interest right from the start to ensure the utilization of poultry flock in a house as the study unit as compared to the flock on the farm. After analysis of the data, using both study units, there are some differences in the type of predictor variables selected. However, when one examines the  $R^2$  value or the amount of variability explained by the respective predictor equation, along with the selected predictor variables, the gain in collecting data on a house basis has not been beneficial. We concluded therefore, that the data on a farm basis provide just as much useful predictive information as those based on a house basis and the additional effort and difficulties encountered in gathering data on a house basis did not justify its use as the preferred experimental unit. Instead, from here on, the rest of the data analysis was based using a broiler farm as the study unit.

6.3 Data analysis for developing the predictor model: With the data base given under 6.1, a sequence of BMDP programs were executed in order to develop the final predictor model. The complete set of the data used in the analysis and the printouts from BMDP analytic steps are given in Appendix 4.

6.3.1 Descriptive statistics of variables used in the study:

Detailed basic descriptive statistics were obtained using BMDP2R.

For the initial 141 variables, a summary of basic descriptive statistics is provided in Table 10. Two variables of interest,  $X_{109}$  and  $Y_2$ ; the disease rate based on sample necropsy and average condemnation rate due to diseases observed at processing, served as the response or dependent variables in the predictor model, and were therefore examined closely.

For  $X_{109}$ , there were 75 cases ( $n=75$ ) available for analysis. The mean value of the disease rate for all farms and broods was 2.7%, with a range of 0-11.1% and a variance of 4.9. The histogram of the variable was skewed to the right.

In the case of  $Y_2$ , where  $n=137$ , the mean condemnation rate at processing was 0.68%, with a range of 0.08% to 5.8%. The variance and standard deviations were 0.38 and 0.62 respectively. The histogram of this variable was also skewed to the right, indicating a non-normal distribution curve.

Table 10 Descriptive Statistics for Variables Used in Flock Testing Feasibility Study

Variable	Sample Size (n)	Mean, ( $\bar{x}$ )	Standard Deviation (S.D.)	Minimum	Maximum
X57	138	0.34	0.48	0.00	1.00
X58	138	0.19	0.40	0.00	1.00
X59	138	0.19	0.40	0.00	1.00
X260	138	0.07	0.27	0.00	1.00
X261	138	0.23	0.42	0.00	1.00
X262	138	0.23	0.42	0.00	1.00
X263	138	0.07	0.27	0.00	1.00
X60	138	0.57	0.50	0.00	1.00
X61	138	0.61	0.49	0.00	1.00
X62	115	90.72	1.27	89.00	94.00
X63	123	83.82	1.82	80.00	87.60
X64	77	90.91	1.35	89.00	94.00
X65	132	83.93	2.48	79.80	88.60
X66	139	3.34	0.84	1.00	4.00
X67	139	3.30	0.83	2.00	5.00
X69	139	23.38	3.31	13.00	25.00
X264	139	0.96	0.19	0.00	1.00
X78	139	0.23	0.42	0.00	1.00
X79	139	0.46	0.50	0.00	1.00
X80	139	0.23	0.42	0.00	1.00
X265	139	0.42	0.50	0.00	1.00
X81	139	0.23	0.42	0.00	1.00
X82	139	0.84	0.36	0.00	1.00
X83	139	0.19	0.40	0.00	1.00
X84	137	92.50	46.49	33.00	230.00
X3	138	35145.96	15791.42	14858.00	63818.00
X221	137	34335.69	15488.22	14760.00	63028.00
X222	131	3.75	0.46	1.70	4.30
X7	137	6.61	6.82	0.00	23.00
X8	138	0.42	0.50	0.00	1.00
X9	138	0.50	0.50	0.00	1.00
X10	138	0.57	0.50	0.00	1.00
X14	136	1.92	1.09	1.00	4.00
X15	137	3.65	1.64	1.00	8.00
X16	138	0.84	0.36	0.00	1.00
X17	138	0.19	0.40	0.00	1.00
X18	138	1.36	0.19	0.98	1.98
X19	139	44.69	25.63	0.00	70.00
X20	138	0.84	0.36	0.00	1.00
X22	137	12.07	9.73	0.00	38.00
X23	139	0.88	0.32	0.00	1.00
X24	139	0.96	0.19	0.00	1.00
X25	139	0.88	0.32	0.00	1.00
X26	138	0.26	0.45	0.00	1.00
X27	138	0.34	0.48	0.00	1.00



Table 10 (cont.)

Descriptive Statistics for Variables Used In Flock Testing Feasibility Study  
cont.

Variable	Sample Size (n)	Mean, ( $\bar{x}$ )	Standard Deviation (S.D.)	Minimum	Maximum
X28	138	0.19	0.40	0.00	1.00
X39	136	2.54	0.87	0.95	4.27
X40	128	3.35	1.08	1.80	5.63
X85	137	112.34	47.42	53.00	251.00
X87	133	13.50	7.06	12.00	48.00
X88	139	0.38	0.49	0.00	1.00
X89	138	50.69	3.51	34.00	53.00
X91	136	16131.46	4497.68	9791.00	31660.00
X109	75	2.85	2.70	0.00	11.05
X116	138	0.80	0.40	0.00	1.00
X117	138	0.84	0.36	0.00	1.00
X119	138	0.82	0.31	0.33	1.50
X122	139	0.42	0.50	0.00	1.00
X123	139	0.23	0.42	0.00	1.00
X124	139	0.26	0.45	0.00	1.00
X266	139	0.07	0.27	0.00	1.00
X125	139	4.80	0.80	4.00	8.00
X127	132	317.76	172.02	70.00	600.00
X129	134	0.54	0.33	0.15	1.10
X130	139	8.42	1.41	4.00	10.00
X148	138	40.73	9.99	21.00	53.00
X169	138	0.92	0.27	0.00	1.00
X170	137	0.50	0.50	0.00	1.00
X171	137	0.53	0.50	0.00	1.00
X186	110	1.43	0.41	1.00	2.33
X189	134	0.76	0.42	0.00	1.00
X267	133	0.19	0.40	0.00	1.00
X190	116	2.53	0.92	1.00	4.50
X202	136	77.39	8.99	62.60	90.80
X203	136	65.41	8.90	51.10	80.90
X204	135	53.50	9.26	39.20	71.20
X205	136	4.05	1.09	1.60	5.75
X206	139	0.03	0.19	0.00	1.00
X207	139	0.00	0.00	0.00	0.00
X208	139	0.88	0.32	0.00	1.00
X223	129	32.61	26.14	4.00	80.00
X224	129	0.87	0.61	0.25	2.00
X231	75	7457.30	2333.70	5600.00	15850.00
X235	131	81.69	69.80	10.00	336.00
X237	120	1.07	0.27	1.00	2.00
X241	134	10.26	2.56	6.00	12.00
X245	135	0.92	0.27	0.00	1.00
X247	135	0.42	0.50	0.00	1.00
X248	135	0.23	0.42	0.00	1.00

Table 10 (cont.)

Descriptive Statistics for Variables Used In Flock Testing Feasibility Study  
cont.

Variable	Sample Size (n)	Mean, ( $\bar{x}$ )	Standard Deviation (S.D.)	Minimum	Maximum
X249	135	0.26	0.45	0.00	1.00
X250	135	0.07	0.27	0.00	1.00
X133	111	2.18	2.20	0.53	7.75
Z8	139	0.96	0.19	0.00	1.00
Z9	139	0.30	0.47	0.00	1.00
ZR	138	8.91	1.46	4.50	11.00
TPOP	136	0.02	0.01	-0.00	0.09
X121	139	0.25	0.43	0.00	1.00
X131	102	0.25	0.43	0.00	1.00
X165	119	0.92	0.26	0.00	1.00
X194	77	2.88	1.46	1.00	7.00
X226	83	3.73	1.82	1.00	10.00
X227	84	5.13	2.54	1.00	11.00
X228	84	4.67	2.31	1.00	11.00
X230	89	13.13	3.04	4.00	397.00
X251	135	135453.03	40365.80	81000.00	193200.00
X252	110	123698.18	43530.83	47166.00	248354.00
X253	135	368.47	100.59	250.00	600.00
X254	135	11.62	3.95	8.00	16.00
X255	135	1.45	0.50	1.00	2.00
X110	75	0.00	0.00	0.00	0.00
X111	75	0.00	0.00	0.00	0.03
X112	75	0.02	0.02	0.00	0.12
X113	75	0.00	0.02	0.00	0.66
X114	75	0.00	0.00	0.00	0.02
X115	75	0.00	0.00	0.00	0.35
X132	85	1.06	0.72	0.00	4.17
Y16	118	0.19	0.15	0.02	0.73
Y1	110	0.68	0.42	0.19	2.11
Y2	137	0.91	1.09	0.22	5.80
Y2T	134	0.93	0.78	0.18	3.70
Y3	108	0.01	0.01	0.00	0.09
Y4	108	0.32	0.18	0.00	1.04
Y5	108	0.21	0.32	0.00	1.57
Y6	108	0.13	0.02	0.00	0.11
Y7	108	0.03	0.02	0.00	0.10
Y8	108	0.06	0.06	0.00	0.25
Y9	137	0.01	0.05	0.00	0.57
Y10	137	0.35	0.25	0.07	1.64
Y11	137	0.22	0.50	0.00	5.02
Y12	137	0.01	0.02	0.00	0.12
Y13	137	0.04	0.03	0.00	0.16
Y14	137	0.06	0.07	0.00	0.37
Y15	43	1.60	1.13	0.22	6.49
Y17	130	0.21	0.42	0.00	4.61

Table 10 (cont.)

Descriptive Statistics for Variables Used In Flock Testing Feasibility Study  
cont.

Variable	Sample Size (n)	Mean, ( $\bar{x}$ )	Standard Deviation (S.D.)	Minimum	Maximum
Y9T	134	0.02	0.06	0.00	0.57
Y10T	134	0.39	0.29	0.00	1.65
Y11T	134	0.27	0.56	0.00	5.02
Y12T	134	0.01	0.03	0.00	0.31
Y13T	134	0.03	0.03	0.00	0.15
Y14T	134	0.08	0.12	0.00	0.80

Among the disease specific condemnation rates ( $Y_9$ - $Y_{14}$ ), the mean values for all study farms during the 1981-82 calendar year were 0.01% for leucosis ( $Y_9$ ), 0.35% for septicemia ( $Y_{10}$ ), 0.22% for airsacculitis ( $Y_{11}$ ), 0.0095% for synovitis ( $Y_{12}$ ), 0.036% for tumors ( $Y_{13}$ ), and 0.056% for others ( $Y_{16}$ ). This showed that in terms of importance, as observed in other national figures, condemnation due to septicemia/toxemia and airsacculitis accounted for 83.3% of all whole carcass condemnation due to diseases. In terms of emphasis of developing disease specific condemnation rate models, these two categories will require emphasis as opposed to the others which, at this point, do not appear to be as important.

In an effort to characterize the relationship of the independent and dependent variables, each of the independent variables were plotted against  $Y_2$  and  $X_{109}$ , using BMDP6D. A scatter diagram of each independent/dependent pair is provided in Appendix 4. Amongst the pairs evaluated,  $X_{109}$  VS  $Y_2$  showed the strongest linearity with a correlation coefficient of 0.5888, followed by  $X_{223}$  VS  $Y_2$  and  $X_{224}$  VS  $Y_2$ , which respectively had correlation coefficients of -0.3868 and -0.3720.

Variable  $X_{223}$  represented the distance from the poultry farm to the processing plant, while  $X_{224}$  represented the number of hours for driving from the farm to the processing plant. The rest of the variables did not show strong linearity.

When  $X_{109}$  was the dependent variable and the other independents were plotted against it, the variables with adequate correlation coefficients were the condemnation rate at one previous time period ( $Y_{2t}$ ) with a value of -0.2239, the average fertility rate for the hatchery ( $X_{62}$ ) with -0.2185, average hatchability rate for hatchery ( $X_{63}$ ) with -0.2239, and average hatchability for the brood under study ( $X_{65}$ ) with -0.2182. The rest of the variables did not show satisfactory linearity on the scatter plots.

6.3.2 Comparative statistics to assess differences in condemnation rates among study units: To address the question of whether there were differences in the population means of whole carcass condemnation rates at processing, a number of fixed factor effects were considered. These included mainly, an assessment of differences (by place) among study firms, farms, hatcheries, or (by time) amongst the five brood cycles. Such assessments were performed graphically (figures 15) via tables (11-14) and finally, using analysis of variance (two way layouts).

Figure 15 provides an illustration of the profiles of average mortality rate of poultry and the corresponding average condemnation rate during the five brood cycles and the respective flock sizes. The average mortality rate in the study farms/firms appeared comparative from brood to brood. This also was the case with the average condemnation rate, except during the fourth brood cycle,



Figure 15 COMPARISON OF POPULATION PROFILE FOR FLOCK TESTING STUDY

Tuskegee Institute (1981/82)

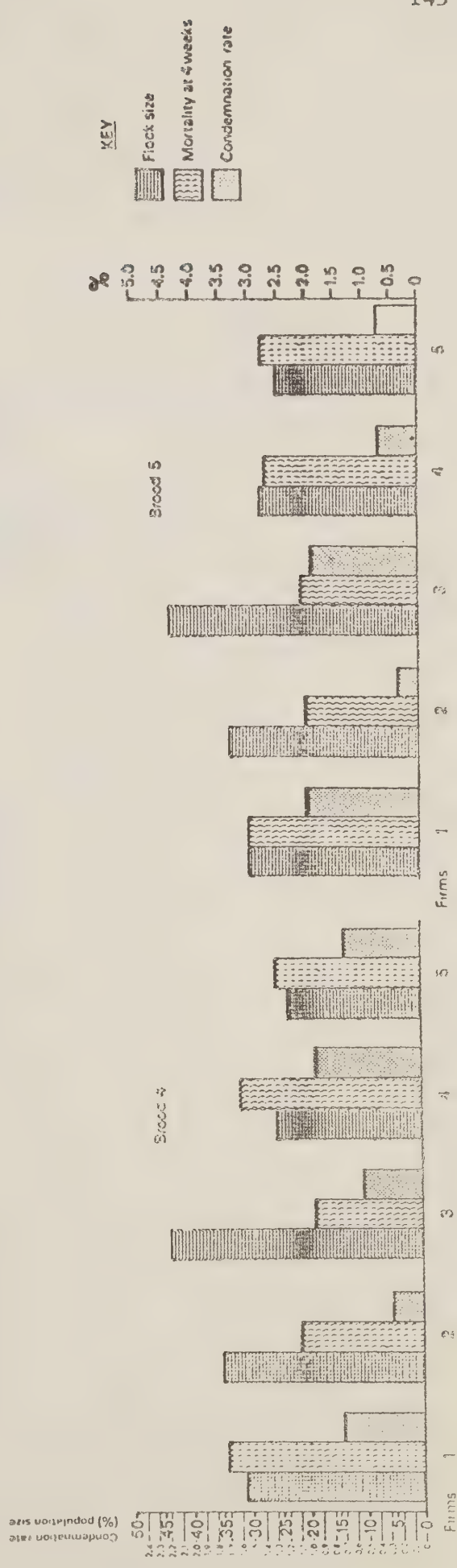
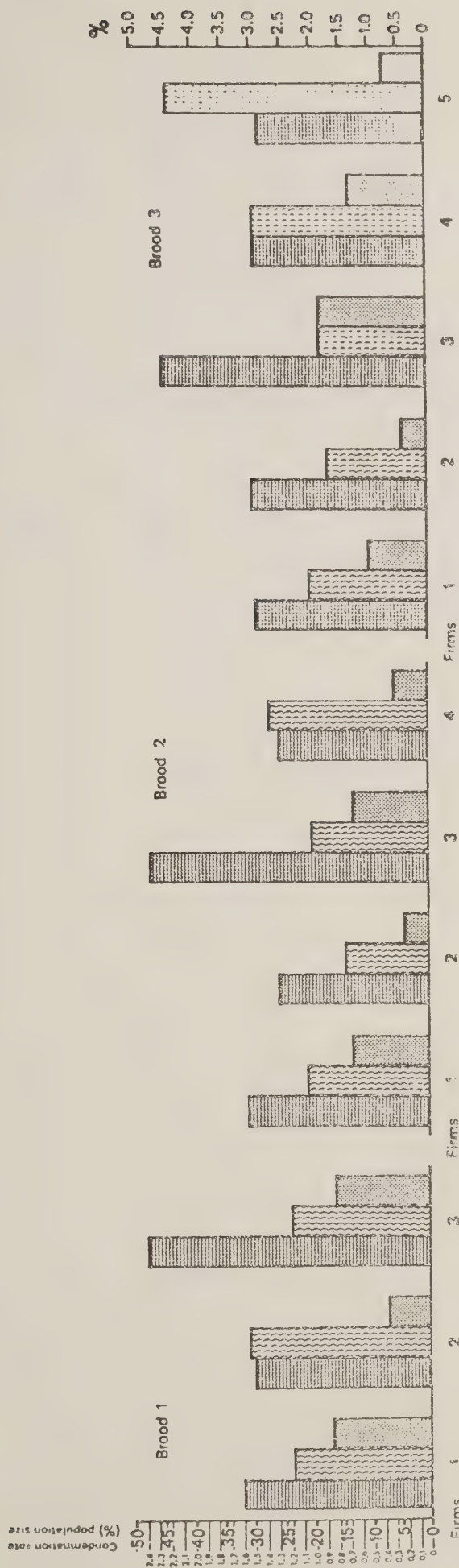


Table 11

Comparison Of Condemnation Rates And Disease Specific Rates  
For Study Firms

	Y2	Y9	Y10	Y11	Y12	Y13	Y14
Firm 1 (All Broods)	0.723	0.029	0.368	0.132	0.018	0.049	0.136
Firm 2	0.259	0.005	0.224	0.012	.003	0.008	0.003
Firm 3	1.014	0.014	0.287	0.599	0.028	0.058	0.047
Firm 4	0.728	0.008	0.540	0.112	.001	0.022	0.053
Firm 5	0.499	0.004	0.370	0.085	.005	0.038	0.0

Table 12 Condemnation Rates for Hatcheries Used In Flock Testing Study (1981/82)

Brood	Hatchery							
	1	2	3	4	5	6	7	8
1	0.649;1.948 1.010;1.302 0.631;0.962 0.672	1.302 0.672	0.255;0.221 0.204;0.232 0.146;0.182	0.138 0.146 0.182	0.934;0.714 1.037;0.658 2.044;0.896 0.488	0.714;1.037 0.658;0.896 0.488	0.551;0.601 0.780;0.444 1.892 0.387	0.550;0.368 0.401;0.263 0.220 0.382
2	0.648;0.542 0.463;1.417	0.508;0.542 0.463;0.450 0.747	0.171;0.543 0.288;0.259 0.282	0.221 0.084 0.282	0.662;1.177 2.703;1.207 0.401;0.817	2.703;1.207 0.477	0.686;1.319 0.940;1.115 1.209;0.380	2.033;0.324 0.330;0.412 0.414;0.321
3	0.720;0.464 0.433;0.425 0.280;0.621 0.460	0.425 0.460	0.231;0.344 0.137;0.239	0.226	1.023	5.800;0.902 1.023;1.002 0.865;0.982	0.314;1.477 1.734;0.296 0.754;0.790	0.470;0.283 0.295;0.836 0.598
4	0.938;0.377 0.494;0.529	0.573;0.742 0.700	0.367;0.243 0.211;0.248 0.114	-	0.674;0.579 0.331	0.797;0.618 0.449;0.868	0.214;0.326 0.232 0.423	-
5	0.936;0.691 1.020;0.603 0.888	0.747;1.020 0.888;0.701	0.368	0.365;0.312 0.559;0.218	-	0.697;0.730 0.617;1.222 0.478;0.905	-	-

Table 13

Various Comparative Parameters For Hatcheries Used In Flock Testing Study (1981/81)

Firms  
↓

Hatcheries → Parameters	A		B		D		E	F	$\bar{x}$	s
	1	2	3	4	5	6	7	8		
Average fertility rate	90.36	90.29	90.86	89.90	90.41	92.17	91.33	-	90.76	0.77
Average hatchability rate	83.04	83.15	85.73	84.10	85.42	84.47	85.60	86.84	84.79	1.33
Mortality rate 4 weeks	2.69	2.84	1.81	2.26	1.98	2.07	3.18	3.10	2.49	0.53
Mortality rate 6-7 weeks	3.36	3.53	2.48	2.97	3.00	3.12	4.33	4.54	3.42	0.70
Disease rate (X109)	2.69	-	1.48	2.58	4.46	4.50	3.17	3.00	3.13	1.07
Condemnation rate (Y2)	0.75	0.72	0.25	0.26	0.95	1.11	0.77	0.50	0.66	0.31

Table 14

Condemnation Rate ( $Y_2$ ) For The Strata Of Study Farms Used In  
Flock Testing Study

Farm/Firm	Good		Average		Poor	
A	0.649	0.280	1.948	0.377	1.302	0.460
	0.631	0.938	1.010	0.742	0.672	0.494
	0.648	0.529	0.962	0.936	0.463	0.700
	1.417	0.747	0.508	0.691	0.747	1.020
	0.720	0.603	0.542	0.888	0.425	0.701
			0.450			
			0.464			
			0.433			
			0.621			
			0.573			
B	0.138	0.243	0.255	0.226	0.204	0.211
	0.212	0.365	0.232	0.367	0.182	0.312
	0.171		0.146	0.248	0.288	0.249
	0.543		0.221	0.114	0.137	
	0.344		0.259	0.368		
			0.084	0.559		
			0.231	0.218		
D			0.239			
	0.934	0.674	1.037	1.023	2.044	0.331
	0.714	0.579	0.658	1.002	0.488	0.868
	0.662	0.697	0.896	0.982	0.401	0.478
	1.177	0.730	2.703	0.797	0.817	
	5.800		1.207	0.618	0.865	
	0.902		0.477	0.449	0.960	
				0.617		
E				1.222		
				0.905		
	0.511	0.214	0.601	0.380		
	0.444	0.423	0.780	1.477		
	0.686		1.892	1.734	None Available	
	1.115		1.319	0.754		
	0.314		0.940	0.326		
F	0.296		1.209	0.232		
	0.550		0.210		0.220	
	0.368		0.263		0.382	
	2.033		0.330		0.414	
	0.324		0.412		0.312	
	0.470		0.295		0.836	
	0.283				0.598	



when it was lower. Note that the comparisons could be made along the horizontal axis, whereby the respective values for each of the five firms and five brood cycle are presented. The five sets of graphs could also be examined vertically, whereby possible differences during the different brood cycles could be examined for each firm, one at a time.

In figure 15, firms A and D showed a higher condemnation rate than the others. The condemnation rates, however, varied from brood to brood and from one study farm or firm to another. In Table 11, the respective percent (%) condemnation rate due to specific diseases is provided for each firm for comparative purposes.

Table 12 presents the values for  $Y_2$ , the condemnation rate for each of the study hatcheries and the corresponding brood cycles which also showed variabilities both by time and place. Table 13 provides comparative values for selected hatchery parameters. Other than providing somewhat superficial profiles of the response variable ( $Y_2$ ), indepth analysis and assessment of the mean differences for this variable could not be performed.

Therefore, such variabilities were examined quantitatively using a fixed effects, two way ANOVA models. The tested hypothesis to examine differences in condemnation rates were:

- test of equality of row means of condemnation

rates ( $Y_2$ )

- test of equality of column means ( $Y_2$ )
- test of no interaction between column and row factors.

The following cases were considered:

- a) to assess if differences existed by place (firms) and by time (brood cycle) the average condemnation rate ( $Y_2$ ) was classified for the two factors, i.e. five levels of firms (A, B, D, E, F) and brood cycles, which had three levels, (Cycle 3, 4 and 5). An analysis of variance was performed (Table 15) and an F ratio of 4.13677 was obtained for the firm factor indicating that there was a statistically significant difference in condemnation rates amongst the five firms at the 95% level of significance ( $F_{0.95, 4, 8} = 3.84$ ). Conversely, there was no statistically significant difference in terms of brood cycles or in interaction between the two factors.
- b. study farm (4 levels) by study firms (5) levels: The condemnation rate ( $Y_2$ ) was cross-classified by study firm and farms. The rows represented firms and columns represented farms. Using a two way ANOVA approach, an F ratio of 3.7007 was obtained for the row factor ( $F_{0.95, 3, 27} = 2.96$ ), while the column factor and interaction showed a non-significant F value.

Table 15 Anova Summary Table for Comparing Performance of Firms

Source	D.F.	M.S.	F-Ratio
Brood Cycle	2	.107542	.294126
Firms	4	1.51253	4.13677
Brood x Firm Interaction	8	.593236	1.6225
Error	76	.365631	
TOTAL	90	.4311	

- c. A similar analysis was conducted for firms A, B and D, but, with the brood cycle factor occurring at 5 levels. For this case an F ratio of 13.3521 was obtained. This was also statistically significant ( $F_{0.95, 2, 8} = 4.26$ ).
- d. Flock size ( $X_3$ ) vs disease rate on necropsy ( $X_{109}$ ): the variable  $X_3$  was divided into three categories viz. farms with ( $X_3$ ) flock size of: 20,000 or less, 20,000 to 40,000 and those with over 40,000 birds. The disease rate ( $X_{109}$ ) was divided into 0.2 or less, 0.2 to 1.0 and greater than 1.0. The result indicated that the F value for row ( $X_3$ ) and a column ( $X_{109}$ ) and interaction, were all insignificant.

It is concluded then that, for the firms studied in this project, both from the graphical analysis as well as the results of ANOVA, there were significant differences in the means of the samples for whole carcass condemnation rates among firms/farms. However, there were no such observable or quantifiable differences over time, i.e. (five brood cycles).

It is important to emphasize here that the ANOVA was performed to provide more comparative information among study units. The basic objective of the study was not comparative in nature, but one which required the development of a predictive model for condemnation rate. Thus multivariate causal models were utilized for such a task

and these will be presented next.

6.3.3 Multivariate analytic methods: The analytic methodology to develop the predictive models for poultry whole carcass condemnations due to diseases were based on linear multivariate models which involved multiple linear regression and discriminant analysis. The rationale for such an approach and the diagrammatic visualization of the static linear causal model which interrelated the predictor variables for condemnation rates (Y) have been given earlier (Figure 12, 13).

For these two models, systematic variable reduction steps to select the best subset of predictor variables, were required. Following the decision-making criteria for variable reduction/deletion (5.10), the data base was examined critically, in steps, to arrive at the final conclusion.

#### 6.3.3.1 Variable reduction phases:

Phase I - Preliminary - Based on criteria given under 5.10, from the 286 original potential predictors, 162 variables were deleted and only 124 independent variables were retained. These variables formed the initial data matrix upon which the various BMDP statistical programs were run. A listing of these initial variables ( $X_k$ ) and the dependent variables retained at the end Phase I, are given in appendix 9. Although, the size of the variable list was substantially reduced, this still left a large number making further reduction necessary.



Phase II - At this point a series of BMDP programs were used specifically to facilitate variable screening. The criteria for selecting and retaining predictor variables during this stage has been presented under methodology.

Unlike the description presented under 6.2, where the analysis was performed using four partitioned matrices, during this last phase of the project, the BMDP program was already modified to handle as many as 200 variables simultaneously. Therefore, no partitioning was required and all the variables, whether for descriptive purposes (P2D, P6D) or regression analysis (P1R, P2R), were handled in one sweep. Specifically, in the case of P1R and P2R, this meant that all potential predictor variables with some influence on the dependent variables ( $Y_k$ ) could be evaluated either individually and/or in combination with others at the same time. Utilizing this method, those with the least influence could then be weeded out with ease, efficiency and with minimal computing cost.

The latter term is used purposely to emphasize that with 4 partitioned matrices, for example, P1R would have had to be run 4 times (one run per partition) while with the non-partitioned case, only one computer run was necessary. This reduced the cost of computation and the time involved in performing the complex set of analysis.

Briefly, during phase II, the BMDP analysis strategy consisted of two steps.

Step 1 consisted of:

- a) Running P2D for all the variables,
- b) Performing P6D and obtaining scatter plots for each of the variables:  $X_{62}-X_{91}$ ,  $X_{125}-Y_{14t}$  vs  $X_{109}$  (the disease rate based on necropsy), each of the variables  $X_{62}-Y_{14t}$  vs  $Y_2$  (condemnation rate).

Only variables which were non-dichotomous were used in these scatter plots.

- c) conducting P1R and P2R for all predictor variables ( $X_{62} - Y_t$ ) with  $X_{109}$  as the dependent variable. When  $X_{109}$  was in use, the disease specific rates corresponding to this variable ( $X_{110} - X_{115}$ ) were omitted from the data matrix. Similarly, the above steps were performed with  $Y_2$  as the dependent variable.

Step 2: Subsequent to the results obtained from step 1, another set of P2R were run for each dependent variable, to further reduce the number of variables. At this stage, the predictor variables selected for retention were based on the results of the stepwise forward and backward stepping sequence of P2R. The final potential predictor variables were further scrutinized at the end of step 2 and the following steps were taken. Although the hatchery source variables were useful predictors of condemnation rates in the study area, since these sources could not be generalized to other areas, hatchery source variables were deleted. Similarly, the indicator variables

for air intake and exhaust directions in the hatchery or broiler house were also omitted.

Therefore, at the end of phase II, the variable reduction task was completed (table 16). Using the predictor variable provided in table 16, two linear multivariate models were developed, one for predictive purposes using BMDP2R, and the other using BMDP7M for classification purposes.

6.3.3.2 Separation of cases into study and test data sets: In order to develop the predictor models and then test or validate the performance of the model, the flock testing study data base was divided into two sets. One of the sets on which the models were developed was referred to as the "study" data base, and the other one as the "test" data set. The "study" data base was composed of all cases in the file, with a complete set of records for each of the variables used in the analysis. The "test" data set were those that had an incomplete set of records but could still be used to validate the final model when a very few set of predictor variables were in use. The point is that, when the number of predictor variables in use were large, the number of cases with a complete record were restricted while if the number of predictors were small, then a larger number of cases were regained. For example, there were a total of 154 cases in the data base in the computer. When developing the predictor model for  $Y_2$ , at the end of phase I, there were only 26 cases with a

Table 16

Variables Selected For Use In Developing Final Predictor Model <sup>a,b</sup>

<u>Dependent Variable</u>	<u>Number of Predictor Variables</u>	<u>Predictor Variables</u>
Y <sub>2</sub>	14	X <sub>60</sub> , X <sub>61</sub> , X <sub>62</sub> , X <sub>63</sub> , X <sub>64</sub> , X <sub>14</sub> , X <sub>109</sub> , X <sub>129</sub> , X <sub>204</sub> , X <sub>205</sub> , X <sub>223</sub> , Y <sub>2T</sub> , X <sub>9</sub> , X <sub>18</sub>
Y <sub>9</sub>	9	X <sub>17</sub> , X <sub>22</sub> , TPOP, X <sub>109</sub> , X <sub>119</sub> , X <sub>205</sub> , Y <sub>2T</sub> , Y <sub>10T</sub> , X <sub>237</sub>
Y <sub>10</sub>	9	X <sub>17</sub> , X <sub>22</sub> , TPOP, X <sub>109</sub> , X <sub>119</sub> , X <sub>205</sub> , Y <sub>2T</sub> , Y <sub>10T</sub> , X <sub>237</sub>
Y <sub>11</sub> ,	23	X <sub>61</sub> , X <sub>62</sub> , X <sub>63</sub> , X <sub>65</sub> , X <sub>85</sub> , X <sub>88</sub> , X <sub>116</sub> , X <sub>119</sub> , X <sub>127</sub> , X <sub>129</sub> , X <sub>189</sub> , X <sub>267</sub> , X <sub>208</sub> , Z <sub>R</sub> , X <sub>9</sub> , X <sub>14</sub> , X <sub>15</sub> , X <sub>19</sub> , X <sub>40</sub> , X <sub>91</sub> , X <sub>130</sub> , X <sub>205</sub> , Y <sub>11T</sub>
Y <sub>12</sub>	14	X <sub>64</sub> , X <sub>65</sub> , X <sub>66</sub> , X <sub>7</sub> , X <sub>14</sub> , X <sub>19</sub> , X <sub>88</sub> , X <sub>125</sub> , X <sub>129</sub> , X <sub>148</sub> , X <sub>133</sub> , Z <sub>R</sub> , X <sub>67</sub> , X <sub>140</sub>
Y <sub>13</sub>	18	X <sub>62</sub> , X <sub>63</sub> , X <sub>65</sub> , X <sub>85</sub> , X <sub>88</sub> , X <sub>119</sub> , X <sub>125</sub> , X <sub>202</sub> , X <sub>224</sub> , X <sub>235</sub> , X <sub>245</sub> , X <sub>133</sub> , Z <sub>R</sub> , Y <sub>2T</sub> , Y <sub>13T</sub> , X <sub>117</sub> , X <sub>190</sub> , X <sub>206</sub>
Y <sub>14</sub>	16	X <sub>61</sub> , X <sub>84</sub> , X <sub>8</sub> , X <sub>19</sub> , X <sub>40</sub> , X <sub>88</sub> , X <sub>109</sub> , X <sub>148</sub> , X <sub>189</sub> , X <sub>267</sub> , X <sub>202</sub> , X <sub>205</sub> , X <sub>208</sub> , X <sub>224</sub> , X <sub>237</sub> , Y <sub>2T</sub>
X <sub>109</sub>	19	X <sub>60</sub> , X <sub>63</sub> , X <sub>65</sub> , X <sub>222</sub> , X <sub>16</sub> , X <sub>17</sub> , X <sub>39</sub> , X <sub>40</sub> , X <sub>88</sub> , X <sub>117</sub> , X <sub>148</sub> , X <sub>189</sub> , X <sub>190</sub> , X <sub>208</sub> , X <sub>206</sub> , X <sub>231</sub> , X <sub>133</sub> , Z <sub>R</sub> , TPOP

Table 16 cont.

Variables Selected For Use In Developing Final Predictor Model <sup>a,b</sup>

<u>Dependent Variable</u>	<u>Number of Predictor Variables</u>	<u>Predictor Variables</u>
X <sub>111</sub>	36	X <sub>57</sub> , X <sub>58</sub> , X <sub>262</sub> , X <sub>63</sub> , X <sub>67</sub> , X <sub>265</sub> , X <sub>82</sub> , X <sub>84</sub> , X <sub>17</sub> , X <sub>27</sub> , X <sub>85</sub> , X <sub>116</sub> , X <sub>117</sub> , X <sub>169</sub> , X <sub>202</sub> , X <sub>203</sub> , X <sub>204</sub> , X <sub>205</sub> , X <sub>235</sub> , X <sub>133</sub> , Z <sub>9</sub> , Y <sub>2T</sub> , Y <sub>10T</sub> , X <sub>59</sub> , X <sub>264</sub> , X <sub>9</sub> , X <sub>14</sub> , X <sub>22</sub> , X <sub>397</sub> , X <sub>91</sub> , X <sub>119</sub> , X <sub>130</sub> , X <sub>189</sub> , X <sub>206</sub> , Z <sub>R</sub> , TPOP
X <sub>112</sub>	13	X <sub>62</sub> , X <sub>63</sub> , X <sub>64</sub> , X <sub>16</sub> , X <sub>119</sub> , X <sub>189</sub> , X <sub>267</sub> , Z <sub>R</sub> , X <sub>61</sub> , X <sub>7</sub> , X <sub>9</sub> , X <sub>40</sub> , X <sub>148</sub>
X <sub>113</sub>	23	X <sub>260</sub> , X <sub>60</sub> , X <sub>61</sub> , X <sub>64</sub> , X <sub>65</sub> , X <sub>67</sub> , X <sub>264</sub> , X <sub>82</sub> , X <sub>7</sub> , X <sub>9</sub> , X <sub>19</sub> , X <sub>22</sub> , X <sub>23</sub> , X <sub>27</sub> , X <sub>28</sub> , X <sub>40</sub> , X <sub>85</sub> , X <sub>116</sub> , X <sub>129</sub> , X <sub>169</sub> , X <sub>205</sub> , Z <sub>9</sub> , Y <sub>12T</sub>
X <sub>114</sub>	16	X <sub>65</sub> , X <sub>79</sub> , X <sub>15</sub> , X <sub>23</sub> , X <sub>125</sub> , X <sub>129</sub> , X <sub>169</sub> , X <sub>171</sub> , X <sub>186</sub> , X <sub>208</sub> , X <sub>223</sub> , X <sub>224</sub> , X <sub>250</sub> , Y <sub>2T</sub> , Y <sub>13T</sub> , TPOP
X <sub>115</sub>	18	X <sub>84</sub> , X <sub>14</sub> , X <sub>15</sub> , X <sub>16</sub> , X <sub>23</sub> , X <sub>91</sub> , X <sub>148</sub> , X <sub>169</sub> , X <sub>170</sub> , X <sub>267</sub> , X <sub>202</sub> , X <sub>205</sub> , X <sub>206</sub> , X <sub>237</sub> , X <sub>245</sub> , Z <sub>9</sub> , Y <sub>14T</sub> , TPOP

<sup>a</sup> The dependent variable X<sub>110</sub>, disease rate due to leucosis based on necropsy had a value of 0 and therefore, not used in this analysis.

<sup>b</sup>  $TPOP = \frac{X_3 - X_{221}}{X_3}$ , where: X<sub>3</sub> = population of poultry on each study farm during the first week  
X<sub>221</sub> = population of poultry of each study farm at the end of 7 weeks.



complete set of records. At the end of phase 2, there were 37 cases. After the final subset of predictor variables were obtained, there were 17 additional cases which were used to validate the model.

Although, the original intention was to divide the data base into study and data sets randomly, this approach was ignored since the number of cases with a complete set of records for all the variables in use were limited. The lack of random allocation of cases should not be a drawback since in the system adopted here, there was no bias in allocating cases to "study" or "test" data sets. This simply was the result of restrictions imposed on the case records themselves. The validation task therefore was performed satisfactorily as planned as is discussed further below.

6.3.3.3 Attempts to improve the model: Upon completion of the selection of the variables to be used in the final predictor model, two techniques were considered to improve the accuracy of the model. These were:

- (a) transformation of predictor variables
- (b) weighted least squares procedures

Transformation of variables: after examination of the scatter plots of independent variables vs the dependent variables obtained from BMDP6D, as well as the correlation matrix from BMDP1R, selected predictor variables were transformed into their respective square root and exponential forms. These variables were  $X_{62}$ ,  $X_{63}$ ,  $X_{65}$ ,

$X_{221}$ ,  $X_{14}$ ,  $X_{39}$ ,  $X_{40}$ ,  $X_{85}$ ,  $X_{87}$ ,  $X_{109}$ ,  $X_{224}$ , and  $X_{235}$ .

The square root transformation of these variables did not substantially improve the absolute values of the correlation coefficient. In the case of transformation to the respective exponential forms, there was a substantial improvement of the correlation coefficient of  $X_{39}$  from 0.0068 to -0.1559. There was a slight increase for the transformed value of  $X_{109}$  too, from 0.4146 to 0.4848. In the case of  $X_{39}$ , although, its exponential form had a much better correlation coefficient, the sign of the coefficient had changed from positive to negative. From a biological aspect, it was felt that the relationship between  $X_{39}$  and  $Y_2$  would be direct. The above described cases were not encouraging enough so as to pursue this time consuming task on all other variables. Therefore, the variable data were used directly without transformations. The second aspect of attempting to improve the accuracy of the model was the use of weighted least squares procedures. This holds a significant position in the data analysis and is covered in detail further below under its own subheading.

6.3.4 Predictor models: The final selection of the "best" subset of predictor variables was accomplished via a computerized stepwise selection process which utilized forward selection followed by backward stepping regression analysis techniques. This, as referred to earlier, was obtained via BMDP2R, with options for providing covariance

and correlation matrices, residual analysis plots and various tabular data useful for evaluating the adequacy of the fitted model.

The results are presented as cases for various types of condemnation rates viz. an overall condemnation rate due to diseases and disease specific condemnation rates. The variables selected for such a final step were either quantitative in nature or were such that the results would be generalized to refer to other regions. Conversely, a more localized result for the study region (Alabama), is also provided. In the latter case, such variables as hatchery sources, processing plants, and others pertinent only to Alabama were used in developing the final models.

6.3.4.1 Predictor models for overall rates: In order to avoid redundancy and reduce the number of mathematical equations used in this section, the following guidelines were followed:

- a) only predictor equations with a multiple coefficient of determination ( $R^2$ ) of greater than 0.50 are presented.
- b) The equations selected were those obtained at the end of the backward stepping routine of P22
- c) Supporting statistics with these equations will be limited to presenting values of the multiple correlation coefficient ( $R$ ), multiple coefficient of determination ( $R^2$ ) and the F ratio. Other useful items, such as the standardized regression coefficients and standard errors of the

regression coefficients, will be presented only for selected cases.

- d) The description or definition of each variable used in the final analysis (X,Y) is in appendix 9.

The strategy in the development of the predictor models, as well as the presentation of these models further below, revolved around:

- a) developing a predictor equation for condemnation rate ( $Y_2$ ) or the respective disease specific rates ( $Y_9 - Y_{14}$ ), using  $X_{109}$  (disease rate based on necropsy) as one of the predictor variables.

One of the important phases of this project was to utilize the available data in order to evaluate the predictive value of  $X_{109}$ . After analysing the data both on a house basis as well as on a farm basis, it was found that the predictive value of  $X_{109}$  was significant. The variable had a strong linear relationship with  $Y_2$  (the condemnation rate at processing), and its coefficients (0.109 on a farm basis and 0.147 on a house basis) appeared relatively stable. This indicated that this variable could be used as a predictor if a practical alternative of sampling birds on the farm 1-2 days prior to shipment to slaughter could be devised. Since the concept of flock testing partly relied on the result of the performance of this variable, it was felt that this finding was very significant.

It is again vital to briefly touch on the idea of why

flock testing and the use of X109 as a predictor is a rational adjunct (conceptually) to poultry inspection by referring to figure 3. Other than processing plant errors, the major determinant of condemnations and the area of responsibility for inspection is that of condemnations due to diseases. In this case, since it is highly unlikely that diseases suddenly arise in transit or while birds are in processing, it is only logical to think that the disease conditions that led to condemnations during inspection must have had some time to develop and be recognized as lesions. In that case then, this must have taken place while the flock was still on the farm. Although the disease rate (variable X109) was determined at the time of slaughter, it could be inferred that X109 would be representative of the disease rate 1-2 days earlier while the birds were still on the farm. Therefore, if a mechanism could be devised to obtain such information prior to slaughter of the flock, a reliable indication for the condemnation rate could be projected.

- b) Although X109 was a significant predictor, the question of how to devise an approach to the random sampling of birds while the birds are still on the farm was raised. One alternative to this problem was to also devise a predictive model for  $X_{109}$  as the dependent variable. This way, one first predicts a value for  $X_{109}$  for a broiler flock to be processed using available



data as prescribed in an equation for  $X_{109}$ . The predictor equation for  $Y_2$  which would have  $X_{109}$  as one of its predictor variables will then be replaced by the predicted  $X_{109}$  value, and an estimate of  $Y_2$  will be computed. Based on  $Y_2$ , decisions may then be made for an appropriate type of inspection.

- c) Weighted least squares equations were used to improve the predictor equations for  $Y_2$ ,  $Y_9$ - $Y_{14}$  and  $X_{109}$ .

The results of the final analysis provided the following predictor models presented under cases 1-3. These equations therefore were the end products of the total effort of the project carried out during 1981-82.

Case 1. Predictor models for study area:

Since the study was centered around the poultry industry in Alabama, some of the variables studied were unique for the region, e.g. hatchery sources. Therefore, the first objective was to present the results of the predictor equations pertinent to the study area. The equation for predicting condemnation rate in the study area was:

$$\hat{Y}_2 = 16.48972 - 0.18201X_{63} + 0.22468X_{109} - 0.46324X_{205} + 0.08781X_{241}$$

$$(R = 0.89, R^2 = 0.79, F \text{ ratio} = 30.83) \quad (1)$$

Where:

$\hat{Y}_2$  = predicted (%) condemnation rate

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{109}$  = average disease rate (%) based on necropsy

$X_{205}$  = total precipitation (in)

$X_{241}$  = number of inspectors in plant

$R$  = multiple correlation coefficient

$R^2$  = multiple coefficient of determination

Correspondingly, the equation for predicting the disease based on necropsy was:

$$\begin{aligned}\hat{X}_{109} = & 39.54751 - 2.91267X_{58} - 2.02945X_{261} - 0.44252X_{65} \\ & + 3.23479X_{27} - 0.55159X_{39} + 1.99651X_{117} + 1.57413X_{169} \\ & + 1.04076X_{189} - 1.8704X_{208} - 1.95384X_{206} - 1.92653Z_6 \\ & + 9.36482T_{\text{pop}} \quad (2) \\ (R = 0.93, R^2 = 0.86, F \text{ ratio} = 15.13)\end{aligned}$$

Where:

$\hat{X}_{109}$  = average disease rate (%) based on necropsy

$X_{58}$  = hatchery source no. 2

$X_{261}$  = hatchery source no. 5

$X_{65}$  = average hatchability rate (%) for brood

$X_{27}$  = location of air exhausts in broiler house  
(NNE)

$X_{39}$  = age specific mortality rate at 4 weeks

$X_{117}$  = type of feed (crumbles)

$X_{169}$  = vaccine manufacturer # 1

$X_{189}$  = litter type 1

$X_{208}$  = season (spring)

$X_{206}$  = season (fall)

$Z_6$  = location of air exhausts in broiler house  
(SSE)

$T_{pop}$  = change in population size from first week to  
week of brood

Two equations are presented above; one for predicting the overall condemnation rate ( $Y_2$ ), and the other for predicting disease rate ( $X_{109}$ ). For any predictor equation, it is essential to examine the types of regression coefficients including their signs and magnitude. In this case, the signs of these coefficients indicated that  $X_{63}$  and  $X_{205}$  had an inverse relationship with the condemnation rate ( $Y_2$ ), e.g. if the average hatchability rate for the hatchery increased, the condemnation rate decreased. This is consistent with the biological reasoning that a hatchery of a firm with good management would lead to a lower condemnation rate at processing. Conversely,  $X_{109}$  and  $X_{241}$  had a direct (positive) relationship with  $Y_2$ . For example, a high disease rate or  $X_{109}$  would correspondingly lead to a high condemnation rate ( $Y_2$ ) at processing. Again, this is consistent with what one would expect with an understanding of poultry population health. A high morbidity rate ( $X_{109}$ ) would necessarily lead to a higher condemnation rate. In the case of  $X_{241}$ , which represents the number of inspectors in a processing plant, the interpretation is two fold. In one case, this means that if there are more inspectors in a plant, they may tend to condemn more due to the fact that they could identify more diseased birds, or, they could make more errors in condemning birds which should

have passed inspection. In both cases, an increase in  $X_{241}$  leads to an increase of  $Y_2$ .

To evaluate the importance or magnitude of each of the regression coefficient in equation 1, it is useful to refer to the corresponding standardized regression coefficients which were:

$$\hat{Y}_2 = -0.415.X_{63} + 0.554X_{109} - 0.529X_{205} + 0.267X_{241} \quad (3)$$

where:

$\hat{Y}_2$  = predicted (%) condemnation rate

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{109}$  = average disease rate (%) based on necropsy

$X_{205}$  = total precipitation (in)

$X_{241}$  = number of inspectors in plant

In this case, direct comparison could be made amongst the predictor variables, and the one with the highest numerical value which would be considered as the most important; the one with the least numerical value, as the least important. Therefore, amongst the four predictor variables, the rankings in terms of importance from highest to lowest were:  $X_{109}$ ,  $X_{205}$ ,  $X_{63}$  and  $X_{241}$ . The effect of  $X_{109}$  and  $X_{63}$  on  $Y_2$  are obvious; however, the importance of  $X_{205}$ , the total precipitation during the brood cycle having an inverse influence on  $Y_2$  may not be easy to explain. One explanation may be that rain cleanses dust particles and the associated organisms in the air so that the risk of exposure to such agents is minimized. Additionally too, during the high rainfall

months in Alabama (late spring and early summer) the combined effect of high precipitation and high temperature may have adverse effect on viral and other agents of concern in poultry production. Therefore as the total precipitation increases, the condemnation rate decreases indicating that the seasonal effect of rainfall on poultry production is an important consideration.

Other pertinent statistics are the multiple correlation coefficient ( $R$ ) and multiple coefficient of determination ( $R^2$ ). Although  $R^2$  measures the proportionate reduction of total variation in  $Y_2$  associated with the use of the set of  $X$  variables, a large  $R^2$  does not necessarily imply that the fitted model is a useful one. In general, though, it is an acceptable measure of the performance of a model in that, the higher the value of  $R^2$  or  $R$ , the more useful of the model. In equation 1, an  $R^2$  of 0.79 indicates that 79% of the variability in  $Y_2$  could be explained using the four predictor variables given. This is quite significant, and when examined the corresponding  $R$  value of 0.89, which indicates the magnitude of the correlation between  $Y_2$  and the four multiple variables, the predictor model appears very satisfactory. Note that one attempts to obtain an  $R^2$  value close to 1.0 or one tries to explain 100% of the variability in the dependent variable. However, in biologically complex processes such as the case studied, an  $R^2$  of 0.79 may be considered very satisfactory.



In light of the above discussion, it was concluded that  $Y_2$ , the condemnation rate of poultry at processing, could be predicted satisfactorily. In a later section, the validity of this model was evaluated via residual analysis and using a test data set.

In general, adding more independent variables in a model inflates  $R^2$ , and it is sometimes useful to utilize a different measure which recognizes the number of independent variables and adjusts for it. This is the adjusted coefficient of multiple determination. In equation 1, the predictor model for  $Y_2$ ,  $R^2$  was 0.79, and the adjusted  $R^2$  was 0.77. It should be noted that only 4 independent variables were used for predicting  $Y_2$ . In the case of equation 2, where 12 independent variables were used to predict  $X_{109}$ ,  $R^2$  was 0.86, while the adjusted  $R^2$  was 0.81. Although there is a slight decrease in the  $R^2$  value, it had not decreased substantially. It also should be pointed out that  $X_{109}$  could be better predicted than  $Y_2$ , as seen from the  $R^2$  and  $R$  values.

The variables useful for predicting  $X_{109}$  were: hatchery source ( $X_{58}$ ,  $X_{261}$ ), average hatchability rate for brood ( $X_{65}$ ), location of air exhausts in broiler house ( $X_{27}$ ,  $Z_6$ ), age specific mortality rate at 4 weeks ( $X_{39}$ ), type of feed-crumbles ( $X_{117}$ ), vaccine source/type ( $X_{169}$ ), litter type ( $X_{189}$ ), season ( $X_{208}$ ,  $X_{206}$ ), and change in population size ( $T_{pop}$ ). With respect to the signs of the regression coefficients, the two hatchery sources out of

eight selected in this model were inversely related to the disease rate  $X_{109}$ . This means that when the source of chicks for one of the study farms was from  $X_{58}$  or  $X_{261}$ , the birds had a lower disease rate and would have a lower condemnation rate at the time of processing. Hatchery sources were represented by indicator variables and therefore, only the presence/absence of specific hatcheries (out of the total of eight used in the study) were considered. This means that in equation 2, the presence of  $X_{58}$  will decrease the disease rate  $X_{109}$  by 2.913 units (%). Location of air exhausts in a broiler house were also handled as indicator variables. In this model, when the direction of air exhausts was to the north, northwest, it was positively correlated with the disease rate ( $X_{109}$ ); while if it was in a south, southeast direction, it had an inverse relationship with  $X_{109}$ . Thus, the location of exhaust fans apparently is significant in affecting the morbidity or disease rate in broiler houses. Although the explanation for it could only be speculated here, in terms of its influence for spreading organisms within the broiler house, this may be an important structural and biological consideration in poultry housing. The other set of indicator variables selected in this model were seasonal factors,  $X_{206}$  and  $X_{208}$ . The signs for these coefficients indicate that the fall or spring seasons are correlated with a lower disease rate. The average hatchability rate of the birds under

study ( $X_{65}$ ) was inversely correlated with  $X_{109}$ . If the chicks at the time of hatching had a high hatchability rate, this was correlated with a lower morbidity rate. The explanation here is that, a high hatchability rate signifies good hatchery management, good genetic stock, a healthy and mature breeder flock that produces stronger baby chicks. In terms of population related factors, the age specific mortality rate at 4 weeks ( $X_{39}$ ) had an inverse relationship with  $X_{109}$ , while the overall population change ( $T_{pop}$ ) was positively correlated with  $X_{109}$ . When the flock size decreases due to mortalities, e.g.  $X_{39}$ , those birds may have died due to some disease and if so, they did not have a chance to stay on and be part of the infected population, which  $X_{109}$  indirectly measures. Conversely, the rate of change in the population size, represented by  $T_{pop}$ ; (viz.: initial population size during the first week, minus the population size at the end of the brood, divided by the initial population size), was positively correlated with  $X_{109}$ . This was consistent in the sense that it accounts for the change in population health which  $X_{109}$  also estimates.

In terms of the comparative importance of the variables used in equation 2, above, an examination of the standardized regression coefficients indicated the following descending rank:  $X_{27}$ ,  $T_{pop}$ ,  $X_{65}$ ,  $X_{58}$ ,  $X_{117}$ ,  $Z_6$ ,  $X_{208}$ ,  $X_{261}$ ,  $X_{206}$ ,  $X_{169}$ ,  $X_{39}$  and finally  $X_{189}$ . Again, the

importance of air exhaust direction, rate of population decline and the average hatchability rate as the top three predictors of disease rate in poultry population are significant points to remember.

The other vital statistics pertaining to the predictor model were the  $R$ ,  $R^2$  and  $F$  ratio, all of which have been given with the predictor equation. The  $R$  for predicting  $X_{109}$  was very high (0.93), and using the 12 variables selected, 86% of the variability of  $X_{109}$  could be explained. This also meant that the model was quite satisfactory in providing reliable values for  $X_{109}$ , which could then be used in predictor equation 1.

In addition to predictor equations for  $Y_2$  and  $X_{109}$ , three other important equations which dealt with disease specific condemnation rates for septicemia, airsacculitis and the "other" disease category were evaluated. These three disease specific rates form more than 80% of the condemnations in processing plants. In this regard all the steps described in the computer analysis of the data were followed in a comparable manner as for  $Y_2$ . The resultant equations obtained at the termination of the bakeward stepping procedure were:

$$\begin{aligned}\hat{Y}_{10} = & 0.11509 - 0.14672X_{58} + 0.07269X_{253} + 0.00368X_{22} \\ & + 0.03661X_{109} - 0.11383Y_{2t} + 0.83637Y_{10T} - 0.09161X_{237}\end{aligned}\quad (4)$$

$$(R = 0.77, R^2 = 0.60, F \text{ ratio} = 10.29)$$

$$\hat{Y}_{11} = 12.81016 - 0.13026X_{63} + 15.138X_{112} - 0.12703Z_R$$

$$-0.16964X_{205} \quad (5)$$

$$(R = 0.79, R^2 = 0.62, F \text{ ratio} = 18.81)$$

$$\hat{Y}_{14} = 0.04641 + 0.03736X_{82} - 0.00023869X_{84} + 0.11217X_8 \\ - 0.00062626X_{19} + 0.000694X_{109} \quad (6)$$

$$(R = 0.86, R^2 = 0.74, F \text{ ratio} = 27.58)$$

Where:

$\hat{Y}_{10}$  = condemnation rate (%) due to Septicemia

$\hat{Y}_{11}$  = condemnation rate (%) due to airsacculitis

$\hat{Y}_{14}$  = condemnation rate (%) due to "other" diseases

$X_{58}$  = hatchery source no. 2

$X_{263}$  = hatchery source no. 7

$X_{22}$  = number of ventrillators

$X_{109}$  = disease rate (%) based on necropsy

$Y_{2t}$  = condemnation rate (%) at one previous brood

$Y_{10t}$  = condemnation rate (%) due to septicemia at one  
previous brood

$X_{237}$  = number of days involved in marketing

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{112}$  = disease specific rate (%) based on necropsy  
(airsacculitis)

$Z_R$  = number of rainy days

$X_{205}$  = total precipitation

$X_{82}$  = location of air exhausts in hatchery (NNW)

$X_{84}$  = date of placing of eggs

$X_8$  = strain group 1

$X_{19}$  = average distance between houses on a farm

The predictor equations for these three rates were not as



good as for  $Y_2$ . Although the disease rate, due to the "others" category, ( $Y_{14}$ ) could be predicted satisfactorily. 74% of the variability in  $Y_{14}$  could be explained by the variables given in equation 6. Each of the variables used in the above equations could be identified using appendix 9. The signs of the regression coefficients, their magnitude or importance, as well as the significance of the  $R$ ,  $R^2$  and  $F$  ratios are comparable to what has been presented above under the discussion for  $Y_2$  and  $X_{109}$ . Although the  $R^2$  values for  $Y_{10}$  and  $Y_{11}$  (septicemia and airsacculitis) were not as high as was hoped for, it still appears satisfactory for providing decision-making information. It is important to point out that, it is better to predict the overall average condemnation rate ( $Y_2$ ) rather than the disease specific rates.

Case 2: Predictor models which could be generalized: In an attempt to develop predictor models for  $Y_2$ ,  $X_{109}$  and condemnations due to disease specific rates ( $Y_9$ - $Y_{14}$ ), variables which appeared to be of local significance were omitted from further analysis. Included in this category were hatchery sources, vaccine sources and location of air intakes or exhausts. Additionally,  $X_{241}$ , the variable representing the number of inspectors working in a processing plant was also omitted since its predictive value may be controversial. The data analysis was

performed in the manner described under methodology.

The predictor models derived in this section were:

$$\begin{aligned}\hat{Y}_2 = & 19.3543 - 0.21023X_{63} + 0.10855X_{14} + 0.20511X_{109} \\ & + 0.3227X_{129} - 0.43571X_{205} - 0.00702X_{223} + 0.18366Y_{2t} \quad (7) \\ & (R = 0.91, R^2 = 0.82, F \text{ ratio} = 19.07)\end{aligned}$$

Where:

$\hat{Y}_2$  = predicted condemnation rate (%)

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{14}$  = total number of strains on farms

$X_{109}$  = disease rate (%) based on necropsy

$X_{129}$  = water spacing per bird (inches)

$X_{205}$  = total precipitation (in)

$X_{223}$  = distance from farm to plant (miles)

$Y_{2t}$  = condemnation rate (%) at one previous brood

$R$  = multiple correlation coefficient

$R^2$  = multiple coefficient of determination

This equation was one which was obtained at the end of the forward stepping regression analysis program. It utilized 7 predictor variables which consisted of average hatchability rate for hatchery ( $X_{63}$ ), the total number of genetic strains of birds on the farm ( $X_{14}$ ), the disease rate variable ( $X_{109}$ ), water spacing per bird ( $X_{129}$ ), total precipitation during the brood cycle ( $X_{205}$ ), the distance from the poultry farm to the processing plant in miles ( $X_{223}$ ) and the average overall condemnation rate at one previous brood cycle. For the variables positively correlated with  $Y_2$ , the

finding is consistent with the underlying biological expectation that one may have. For example, if the previous condemnation rate ( $Y_{2T}$ ) was high, one may expect the current condemnation rate or the response variable ( $Y_2$ ) to also be high.

In the case of the positive relationship between  $X_{14}$  and  $Y_2$  which indicate that if the number of genetic strains in a poultry farm are large, this leads to high condemnation rates. This of course could be a reflection of limitations in the management or that the chances of getting poor doers from among a larger genetic pool is greater than that from a few which would have been selected intentionally for good performance. A similar management related argument could be made for  $X_{129}$ .

The variables with an inverse relationship,  $X_{63}$ ,  $X_{205}$  and  $X_{223}$  are not so straightforward to explain except for the first case. If the hatchability rate ( $X_{63}$ ) is high, this certainly could be indicative of good management and therefore the returns in lower condemnation rates at processing for the firm may be expected. The model indicates that the total precipitation during the brood cycle ( $X_{205}$ ) is inversely related to condemnation rate. Although this could be questionable, one reason here is that significant precipitation is observed during the spring or early summer months in Alabama which may be

the most conducive time for raising poultry with less problems of infectious diseases. The variable for distance from the farm ( $X_{223}$ ) is somewhat peculiar in the sense that one would in fact expect to see a positive influence of  $X_{223}$  on  $Y_2$  i.e. as the distance increases, the birds are exposed to more stress due to travel which may then exasperbate existing abnormalities leading to higher condemnation rates.

However, the relationship in the model was inverse. This can only be speculated here in that possibly due to the fact that transit stress is known to be harmful to animals in general the management may provide good care at the time of transporting of birds to the plants. For an examination of the standardized regression coefficients, the following model is presented:

$$\begin{aligned}\hat{Y}_2 = & -0.480X_{63} + 0.121X_{14} + 0.506X_{109} + 0.109X_{129} \\ & -0.498X_{205} - 0.204X_{223} + 0.0145Y_{2t} \quad (8) \\ (R = & 0.91, R^2 = 0.82, F \text{ ratio} = 19.07)\end{aligned}$$

Where the variable names are as described above under equation 7.

Note that in terms of comparative importance,  $X_{109}$  is the most valuable predictor followed by  $X_{205}$ ,  $X_{63}$ ,  $X_{223}$ ,  $Y_{2T}$  and finally  $X_{14}$  and  $X_{129}$ .

For predictor equations 7 and 8, the  $R$  and  $R^2$  values were 0.91 and 0.82 respectively. This is a very high correlation coefficient and the equation successfully explained 82% of the variability in  $Y_2$ . It also had a significant  $F$  ratio of 19.07 which showed strong linearity between  $Y_2$  and the independent variables. Table 17 provides other useful statistics such as the standard errors of the regression coefficients, the adjusted  $R$  squares and other such data. Based on these, confidence interval estimation and specific hypothesis testings could be



Table 17  
Regression Statistics For Equation 8

Multiple R	0.9064
Multiple R-Square	0.8215
Adjusted R-Square	0.7784
STD. Error of Est.	0.4538

Analysis Of Variance

	Sum Of Squares	DF	Mean Square	F Ratio
Regression	27.493883	7	3.927698	19.07
Residual	5.9732733	29	0.2059749	

Variables In Equation

Variable (Y-Intercept	Coefficient 19.35430)	Std. Error of Coeff.	Std. Reg. Coeff.
X63	-0.21023	0.0428	-0.480
X14	0.10855	0.0922	0.121
X109	0.20511	0.0357	0.506
X129	0.32270	0.3197	0.109
X205	-0.43571	0.0885	-0.498
X223	-0.00702	0.0034	-0.204
Y2T	0.18386	0.1458	0.146

conducted to further scrutinize the performance of the model. At this stage though, it is significant to note that this predictor equation for  $Y_2$  was the best thus far. One reservation to be raised here is that with the rest of the predictor models, the selection of the equation was made at the end of the regression analysis. In this case, the equation was selected at the end of the forward stepping procedure, which meant that some of the variables entered into the equation could be removed during the backward stepping procedure allows that some of the variables entered into the equation be removed during the backward stepping phase of the computer analysis if necessary. That in fact was the case below where:

$$\begin{aligned} \hat{Y}_2 = & 18.22799 - 0.18983X_{63} + 0.22865X_{109} - 0.44509X_{205} \\ & - 0.00858X_{223} \end{aligned} \quad (9)$$

( $R = 0.89$ ,  $R^2 = 0.79$ ,  $F \text{ ratio} = 29.99$ )

Where:

$\hat{Y}_2$  = predicted condemnation rate (%)

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{109}$  = disease rate (%) based on necropsy

$X_{205}$  = total precipitation (in)

$X_{223}$  = distance from farm to plant (miles)

Again this equation is quite good although its  $R$  and  $R^2$  values are slightly less than in equation 8. The  $F$  ratio shows much stronger linearity. In both cases, the number of predictor variables are of small

size and therefore manageable and easy to explain.

Predictor equations for the six categories of disease specific rates ( $Y_2 - Y_{14}$ ) were also evaluated. However, these were not as satisfactory as was the case for  $Y_2$ . The next step was to develop a predictor model for  $Y_{109}$ ; the disease rate based on necropsy. This variable was an indicator of morbidity on a farm. The predictor equation of  $X_{109}$  for the generalizable model was:

$$\begin{aligned} \hat{X}_{109} = & 56.540079 + 0.7358X_{60} - 0.63653Y_{63} + \\ & 0.0542X_{148} + 0.54026Y_{190} - 2.41932Y_{208} - \\ & 1.92399Y_{206} + 0.2509X_{123} - 0.21801Z_0 + \\ & 2.89333T_{pop} \end{aligned} \quad (10)$$

( $R = 0.78$ ,  $R^2 = 0.60$ ,  $F \text{ ratio} = 5.3^\circ$ )

This model did not appear as satisfactory, although its  $R$  value of 0.78 was acceptable. Due to the fact that the equation was not deemed satisfactory for this work, detailed discussions of the variables has not been presented. Instead, an attempt was made to improve the predictor equation via weighted least squares procedures as described under Case 3.

- 6.3.4.2 Case 3: Weighted least squares: A two stage least squares procedure was used to accomplish this task. Firstly, using equations 1-7, the predicted values for the  $Y$ 's for each of the study cases were obtained. Secondly, the estimates for the weights to be used for each study case were computed. These estimated weights

were then used to obtain the weighted least squares regression model. It should be noted that this discussion applies to the generalized model. The weighted regression model was:

$$\begin{aligned} \hat{Y}_2 = & 4.8499 - 0.05184X_{62} + 0.15089X_{14} + 0.05382X_{109} + \\ & 0.14903X_{129} + 0.03337X_{205} - 0.00365X_{223} + \\ & 0.10326Y_{2T} - 0.34003X_9 \quad (11) \\ (R = 0.93, R^2 = 0.86, F \text{ ratio} = 11.02) \end{aligned}$$

This equation was obtained at the end of the forward stepping program of BMDP2R. The variables with positive correlations with  $Y_2$  were: the number of poultry genetic strains on the farm ( $X_{14}$ ), the estimated disease rate of flock ( $X_{109}$ ), water spacing per bird ( $X_{129}$ ), the total precipitation for the brood ( $X_{205}$ ) and the condemnation rate for one previous brood ( $Y_{2T}$ ). Those with a negative influence on  $Y_2$ , were: the average fertility rate for the hatchery ( $X_{62}$ ), the distance between the farm and the processing plant ( $X_{223}$ ) and type of strain- ( $X_9$ ). Except for  $X_9$ , the interpretation of the variables selected above have been discussed earlier under Case 2. The weighted least squares model indicated that the presence of strain type 1 birds is good in the sense that a fewer percent of these would be condemned at processing.

The standardized regression coefficients of this model indicated that comparatively,  $X_9$  and  $X_{14}$  were

the most important variables followed by  $X_{109}$ ,  $X_{223}$ ,  $Y_{2T}$ ,  $X_{129}$ ,  $X_{62}$  and finally  $X_{205}$ . The  $R$  and  $R^2$  values were very good although the  $F$  ratio was not as strong. With the aid of weighted least squares, the accuracy of the model as measured by  $R$  and  $R^2$  had increased some but not very substantially.

Therefore, in predicting  $Y_2$  for a generalized model, either the weighted least squares approach or the one given under Case 2 were satisfactory and comparable. In a similar fashion, a weighted least squares model for  $X_{109}$  was derived where:

$$\begin{aligned} \hat{X}_{109} = & 27.61194 - 0.37163X_{63} + 0.1091X_{148} + \\ & 0.36292X_{133} \end{aligned} \quad (12)$$

( $R = 0.999$ ,  $R^2 = 0.0997$ ,  $F$  ratio = 117.07)

The predictor equations selected were average fertility rates for the hatchery supplying chicks to the farm ( $X_{63}$ ), the duration in days of prophylactic medications ( $X_{148}$ ), and the average feed utilization rate at the end of seven weeks ( $X_{133}$ ). The model indicated that the longer the duration of prophylactic medication, the higher the estimated value for disease rate in the flock. This is somewhat understandable in that if the flock of birds is kept in a healthy, well-managed environment, prophylactic medications may be used in a planned and judicious manner so that only the least needed time span will be utilized. If the flock is generally unhealthy,



the duration of prophylactic medications will be longer. Therefore, this variable ( $X_{148}$ ) does not indicate a biologically reasonable influence on  $X_{109}$ . In the case of feed utilization rate at 7 weeks ( $X_{133}$ ), the positive correlation with  $X_{109}$  may be indicative of mismanagement of feed utilization. The most plausible explanation is that if the flock of birds is healthy, they will tend to consume more and gain more weight in the process. If the birds are healthy, one would expect to see a lower disease rate and an inverse influence on  $X_{109}$ . In this case,  $X_{133}$ , the feed utilization rate was positively correlated to  $X_{109}$  and one possible explanation may involve a mis-management of feed. Although the records of feed delivered during the brood cycle may be large and therefore the feed utilization rate could be high; the effective utilization of the feed by the birds may not be optimal. The explanation for the inverse relationship with fertility rate of the hatchery ( $X_{63}$ ), as pointed out earlier, relies on the premise that a well managed hatchery will show a higher fertility rate and hatchability rate in its chicks. These chicks either come from good genetic stock or the hatching process is well managed leading to lower health risks and lower disease rate later; since the birds get a good start during the most susceptible periods in their lives.

In the weighed least squares model for  $X_{109}$  the  $R$  and  $R^2$  values increased from 0.77 and 0.60 respectively to 0.99 and 0.99 for each of the two parameters. The  $F$  ratio increased from a weak linear value of 5.38 to a strong  $F$  value of 117.07. In short, the least squares model was the best predictor for  $X_{109}$  and therefore recommended as an effective predictor equation.

6.3.5. Discriminant models - to perform the analysis for

developing the linear discriminant functions to classify a flock into high or low condemnation groups at the time of processing, various decision making options were tried. These included criteria for high or low condemnations set at 5%, 2%, 1%, 0.5% and 0.1%. These demarcations were set somewhat arbitrarily but with the idea of providing FSIS with a variety of options for consideration.

The dependent variable used to develop the discriminant models was  $Y_2$ . The analysis was performed using BMDP71; a stepwise discriminant analysis program useful for such tasks. The  $F$ -to-enter and  $F$ -to-remove values were set at 4.0 and 3.996 respectively. For the two categories of condemnation rates (high or low), prior probabilities were set at 0.5.

For the dependent variable  $Y_2$ , the set of classification functions to be used at each demarcation point for high or low condemnation categories, as well as, the correct classification probabilities will be presented

in sequence. Then, one generalized discussion with interpretations directed at one of the classification functions will follow. This should suffice to present the reader with the basic concepts and applications required to understand and infer what needs to be done with the other functions.

a) Demarcation between high and low condemnation rate set at 5%:

$$LC = -2061.35985 + 46.30182X_{63} - 6.5989X_{109} - 77.21999X_{129} + 67.26443X_{205} \quad (13)$$

$$HC = -1639.04883 + 41.10843 - 2.87306 - 64.26469X_{129} + 56.15462X_{205} \quad (14)$$

Percent correct classification overall - 100

Percent correct classification for cases under 5% - 100

Percent correct classification for cases over 5% - 100

b) Demarcation between high and low condemnation rate set at 2%:

$$LC = -2061.35985 + 46.30182X_{63} - 6.5989X_{109} - 77.21999X_{129} + 67.26443X_{205} \quad (15)$$

$$HC = -1639.04883 + 41.10843X_{63} - 2.87306 - 64.26469X_{129} + 56.15462X_{205} \quad (16)$$

Percent correct classification overall = 100

Percent correct classification for under 2% = 100

Percent correct classification for over 2% = 100

c) Demarcation between high and low condemnation rate set at 1%:

$$LC = -4091.15234 + 114.77283X_{60} + 47.4403X_{61} +$$

$$\begin{aligned}
& 44.89483X_{63} + 44.96988X_{64} - 18.59022x_{14} + \\
& 11.94752X_{109} + 48.13914X_{205} - 4.75752Y_{2T} + \\
& 34.62482X_9
\end{aligned} \tag{17}$$

$$\begin{aligned}
HC = & - 3969.55249 + 107.6714X_{60} + 44.38445X_{61} + \\
& 44.18753X_{63} + 44.3899X_{64} - 17.56498X_{14} - \\
& 12.64814X_{109} + 45.09671X_{205} - 0.93103Y_{2T} + \\
& 31.05351X_9
\end{aligned} \tag{18}$$

Percent correct classification overall = 91.9

Percent correct classification for under 1% = 93.1

Percent correct classification for over 1% = 87.5

d) Demarcation set at 0.5%:

$$\begin{aligned}
LC = & - 4863.71973 + 78.50391X_{60} + 77.2642X_{62} + \\
& 28.68534X_{64} - 85.92729X_{129} - 8.73708X_{205} + \\
& 1.32762X_{223}
\end{aligned} \tag{19}$$

$$\begin{aligned}
HC = & 4699.33447 + 76.82549X_{60} + 75.84322X_{62} + \\
& 28.30284X_{64} - 83.62469X_{129} - 7.79638X_{205} + \\
& 1.21027X_{223}
\end{aligned} \tag{20}$$

Percent correct classification overall = 94.6

Percent correct classification for under 0.5% = 88.2

Percent correct classification for over 0.5% = 100

e) Demarcation set at 0.2%:

$$LC = - 5.14413 + 0.11869X_{223} \tag{21}$$

$$HC = - 1.55803 + 0.05232X_{223} \tag{22}$$

Percent correct classification overall = 78.4

Percent correct classification for under 0.2% = 75.8

Percent correct classification for over 0.2% = 100

f) Demarcation set at 0.1%:

$$LC = - 6.00129 - 2.8138X_{61} + 1.42193X_{129} + 0.12364X_{223} \quad (23)$$

$$HC = - 4.25845 + 4.61612X_{61} + 7.37266X_{129} - 0.00404X_{223} \quad (24)$$

Percent correct classification overall = 97.3

Percent correct classification for over 0.1% = 97.2

Percent correct classification for under 0.1% = 100

where:

LC = the equation for classifying a farm into low condemnation category

HC = the equation for classifying a farm into high condemnation category

$X_{63}$  = average hatchability rate (%) for hatchery

$X_{109}$  = disease rate (%) based on necropsy

$X_{129}$  = water spacing per bird (in)

$X_{205}$  = total precipitation (in)

$X_{60}$  = incubator type 1

$X_{61}$  = incubator type 2

$X_{64}$  = average fertility rate (%) for brood

$X_{14}$  = total number of strains on farm

$Y_{2T}$  = condemnation rate (%) at one previous brood

$X_9$  = strain group 2

$X_{62}$  = average fertility rate (%) for hatchery

$X_{223}$  = distance from farm to plant (miles)

In each of the six discriminant models given above, a classification function to specify whether a flock should be categorized into a high condemnation (HC) or low



condemnation (LC) group are provided. These equations were coupled with the respective correct classification probabilities.

Using the classification functions provided, a flock is assigned to the group (HC or LC) with the largest value of the classification functions. For example, for Case 1, the following values are given:  $X_{61} = 1$ ,  $X_{129} = 0.32$ ,  $X_{223} = 12$ . From the LC equation where the demarcation for high/low condemnation is at 0.1%, Case 1 will have a computed value of -6.88. For the HC equation, its computed value will be 2.67. Therefore, since the HC equation had the largest value, the case is assigned to a high condemnation category. All other cases were handled in a similar manner.

In this classification function, the probability of correctly classifying a flock into high condemnation category was 97.2%, for classifying into low condemnation probability of 97.3%. This indicated that the accuracy of the model in providing decision making information was extremely high and very reliable. All the classification functions given under the discriminant models had very high probabilities of correct classification, except for one case viz. the probability of correct classification when the demarcation was 0.2% between high and low condemnation rates. This was only in the higher 70's percentage range, and it was considered less satisfactory than the other 5 cases.

#### 6.4. Selection of the final models

##### 6.4.1. Analysis of residuals

To detect model deficiencies in regression analysis, a simple and effective method was to examine the residuals given by:

$$\epsilon_i = Y_i - \hat{Y}_i$$

The  $Y_i$  are the observed values of the dependent variable; the  $\hat{Y}_i$  are the predicted values obtained by using the given predictor equations. The difference between the observed and the predicted ( $Y_i - \hat{Y}_i$ ) provided the values for the respective residuals ( $\epsilon_i$ ). Corresponding to each  $\epsilon_i$ , in the computer regression analysis, standardized residuals ( $\epsilon_{is}$ ) were computed using:

$$\epsilon_{is} = \epsilon_i / s$$

where  $s$  is the standard deviation of residuals. The standardized residuals have zero mean and unit standard deviation. With a moderately simple sample, these residuals should be distributed approximately as independent normal deviates. An appropriate graph of the residuals will often expose gross model violations if these were present. In general, when the model is correct, the standardized residuals tend to fall between 2 and -2 standard deviations and will be randomly distributed about the zero mean. The residual plots should show no distinct pattern of variation which would

indicate an inherent deficiency in the model. This may indicate inadequacies in the underlying assumptions or errors in the specified equations.

Since an essential part of any regression analysis includes a careful examination of residuals to ensure that the assumptions of least squares theory were fulfilled, residuals of two of the predictor models (equations 7 and 12) were scrutinized with the aid of computer plots (figures 16, 17). Three plots were utilized in each case. In the first one, the objective was to examine the distribution of  $\epsilon_i$  about the mean zero. In both figures, 16 and 17, a plot vs the predicted  $\hat{Y}_i$  indicated that indeed the residuals appeared to be randomly distributed around the zero mean in a balanced manner in about half of the cases i.e. about half of the cases were positive (above 0), the rest were negative (below zero). Note also that the residuals were all within the acceptable standard deviation value of + 2.0. Therefore, this test criteria was satisfactory for the predictor models of  $\hat{Y}_2$  and  $\hat{X}_{109}$ . In the second plot (figures 18, 19), the squared value of the residuals  $(\epsilon_i)^2$  were plotted vs the predicted  $\hat{Y}_i$ . This was expected to show a clustering of most of the  $\epsilon_i^2$  close to zero, the graph did indicate it to be so. When there are outliers, when the residual term is squared, these will be exaggerated and could be picked up from the plots. In these two predictor equations, since the residual deviated within the acceptable range of + 2,

Fig. 16 NORMAL PROBABILITY PLOT OF RESIDUALS

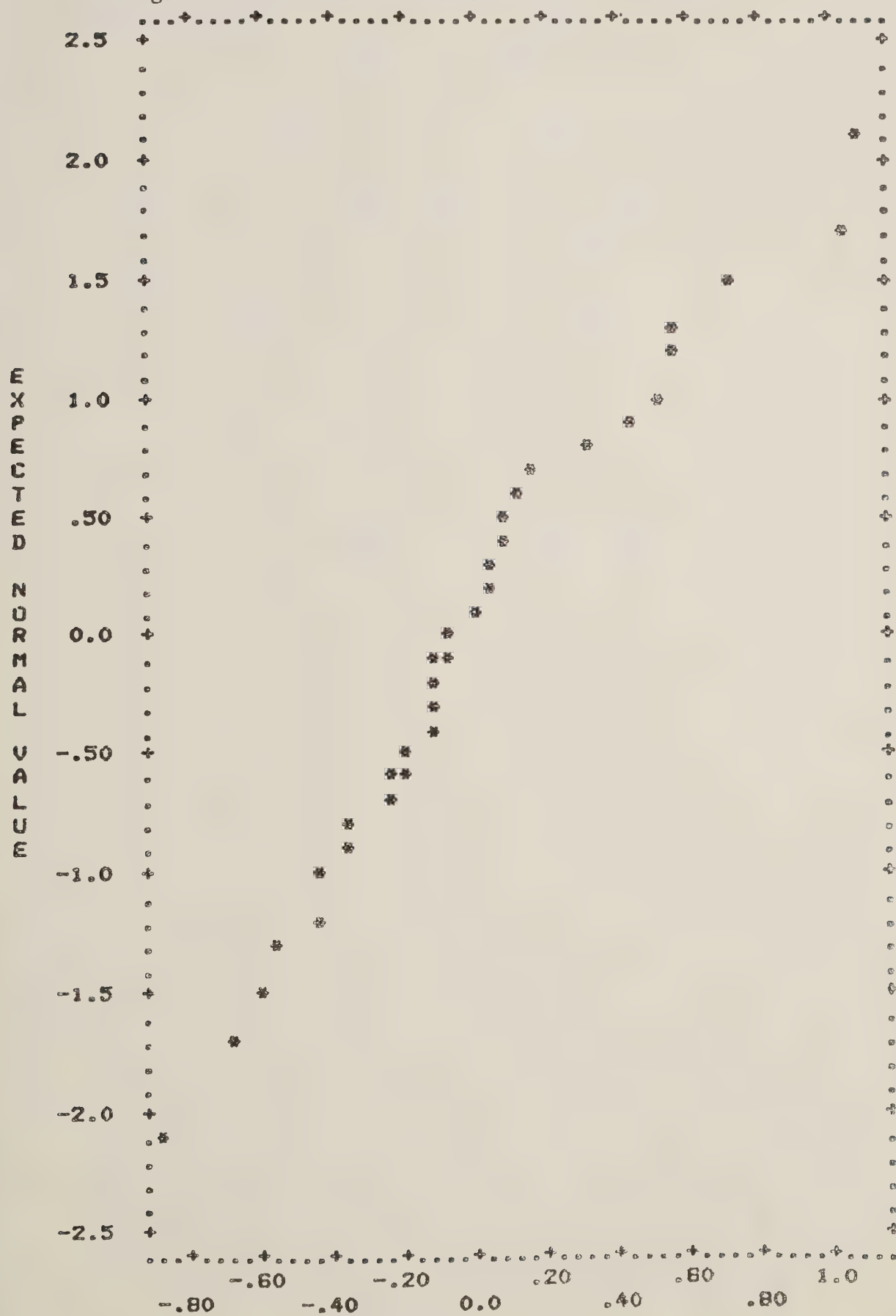


Fig. 17: Analysis of Residuals





there were no major problems with outliers and in terms of model inadequacy.

The third part of the residual analysis involved the examination of a normal probability plot of the residuals (figures 18, 19). In this case, the residual  $(Y_i - \hat{Y}_i)$  was plotted against the expected normal deviate corresponding to its rank. The result of the plot was expected to indicate a linear pattern. Such, of course, was the case for both equations to predict  $\hat{Y}_2$  or  $\hat{X}_{109}$ .

In this case then, with the aid of the three graphical analysis of the residuals, the predictor equations, for  $\hat{Y}_2$  and  $\hat{X}_{109}$  were found to be satisfactory and acceptable. Since the model was developed using "study" data set, the second data set referred to as "test" data set was utilized to validate the model. There were 37 cases in the study data set and 17 cases in the test data. Using test data, only 2/17 of the cases were predicted unsatisfactorily, (standard deviation greater or lesser than 2.0). On the other hand if  $\hat{X}_{109}$  was predicted first using equation 12, and then its value used in equation 7 to predict  $\hat{Y}_2$ , 5/55 cases were predicted to have a standard deviation greater or lesser than 2.0. The rest of the predicted values were with reasonable ranges. In a form of brief comparative statistics, the mean value for observed  $Y_2$  was 0.677%, while for the predicted  $\hat{Y}_2$ , it was 0.768%. Therefore overall, both models performed satisfactorily and the validation process confirmed this.

Fig. 18 NORMAL PROBABILITY PLOT OF RESIDUALS

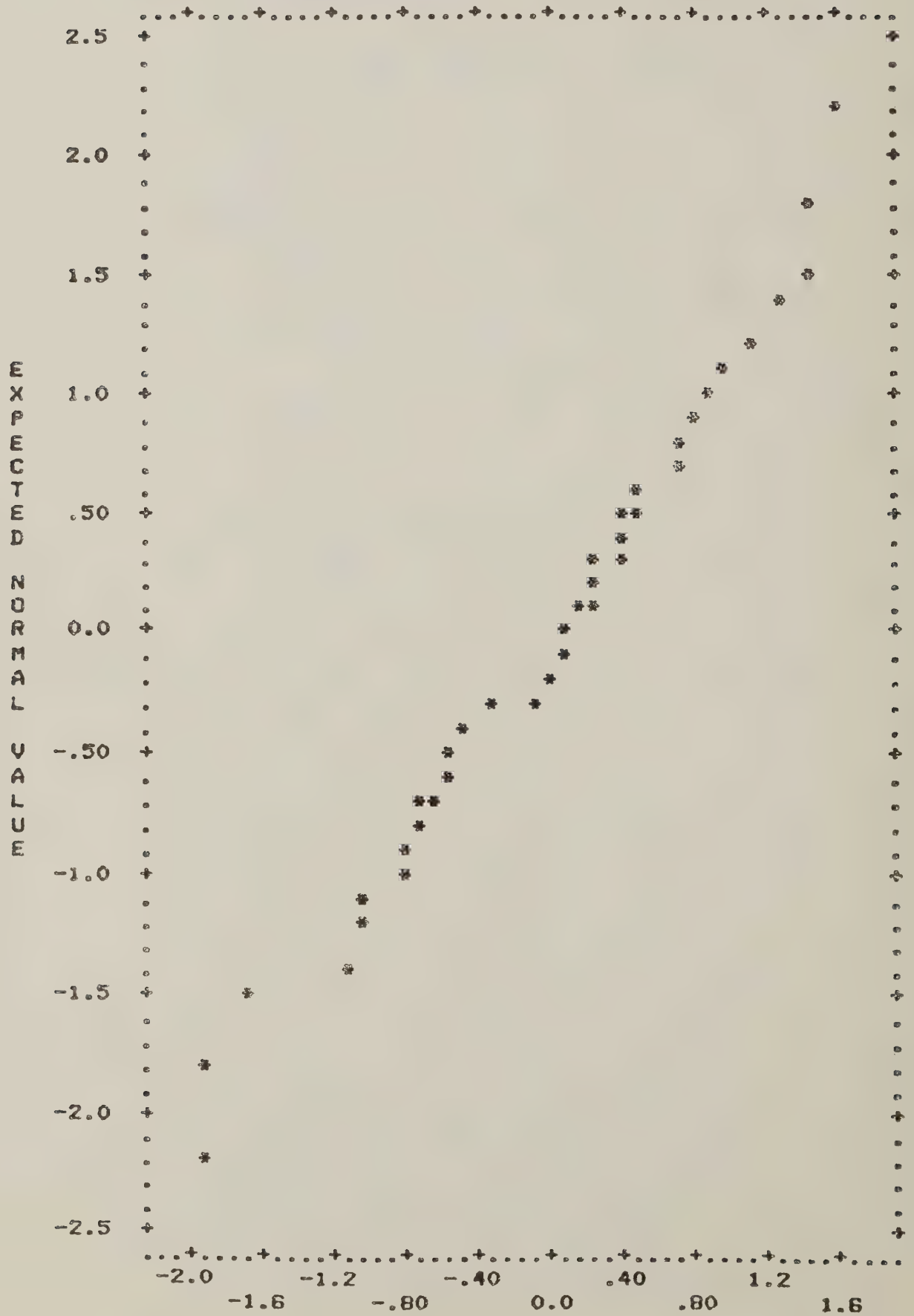
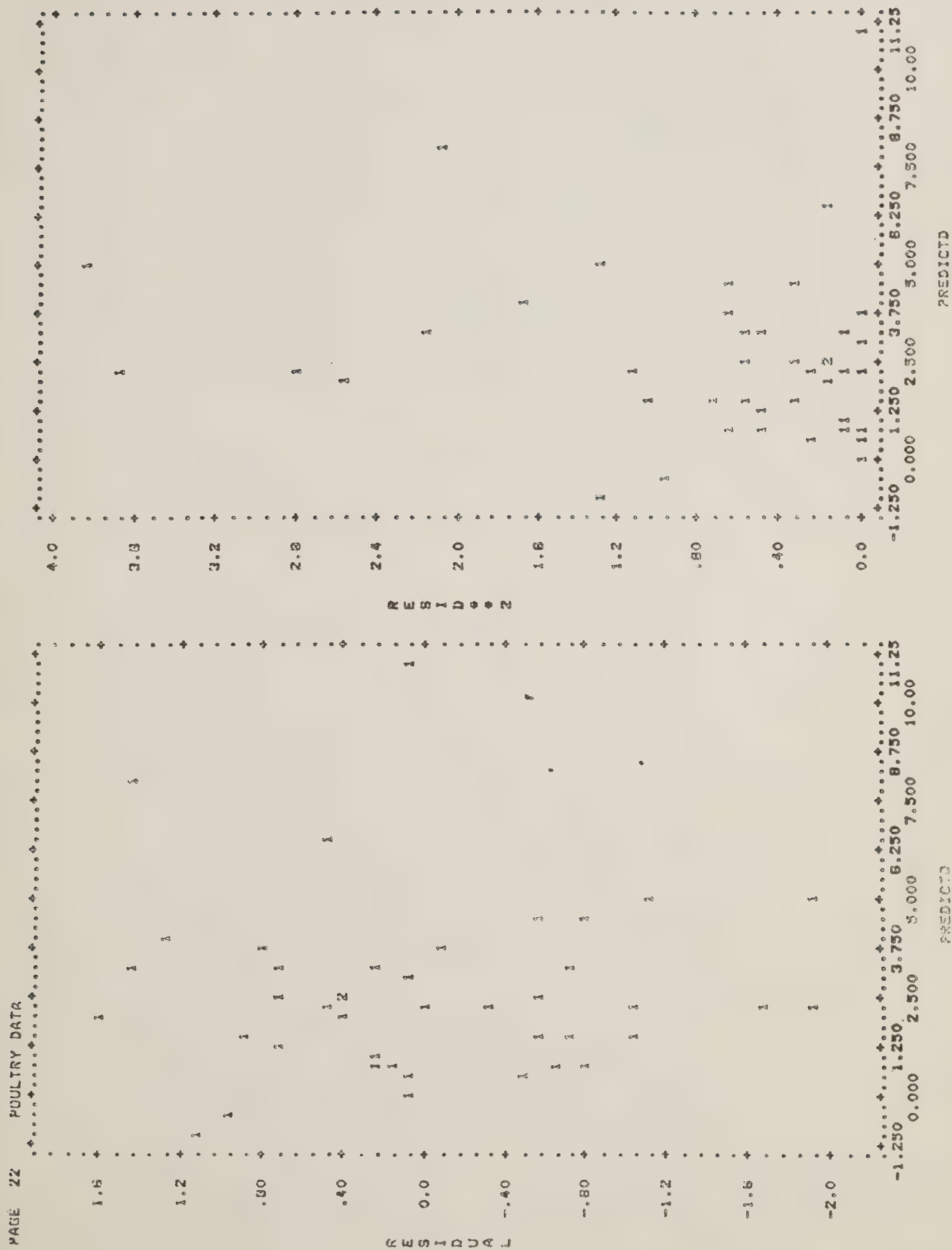


Fig. 19: Analysis of Residuals



The only other follow-up could be validation of these models using independent data from other regions.

One important consideration in performance and validation of the model was an examination of the regression coefficients to see within what limits their parameter values would lie. Therefore, construction of confidence intervals for the coefficients were essential. The 95 percent family of confidence intervals (CI) between two numbers for each regression coefficient where the population parameters could reasonably be expected to lie were computed. These were:

- (a) For the predictor equation of  $\hat{Y}_2$ ; the confidence intervals for the regression coefficients:

$$\beta_{63} = -0.21, -0.123$$

$$\beta_{14} = -0.08, 0.297$$

$$\beta_{109} = 0.132, 0.278$$

$$\beta_{129} = 0.331, 0.977$$

$$\beta_{205} = 0.619, 0.257$$

$$\beta_{223} = 0.014, 0.014$$

$$\beta_{Y_{2T}} = 0.014, 0.482$$

- (b) For the predictor equation of  $X_{109}$ , the confidence intervals for the regression coefficients were:

$$\beta_{63} = 0.372, -0.155$$

$$\beta_{148} = 0.091, 0.127$$

$$\beta_{133} = 0.281, 0.445$$

#### 6.4.2. Validation of Models

In summary both the analysis of the residuals and the

validation of the model using "test" data set indicated that the predictor models would be satisfactory. Additionally, the 95% family of confidence intervals have been provided for each equation to provide information on the range of values within which one would reasonably be confident to find the true or population parameter of the regression coefficients.

#### 6.5 Application of results to poultry inspection

It should be noted that the objective in this study was to develop a predictor model which could serve as an adjunct to the existing poultry inspection procedures and standards. Therefore, the results presented so far are visualized in terms of whether a decision pertaining to the current inspection procedure is to be made in light of information provided by models provided herein. The decision to be made may involve either a "scaled down" inspection, or to maintain the status quo as made operational in the various processing plants.

In order to effectively utilize the models developed in this project, two alternatives are presented. Regardless of the alternative though, two prerequisites for the successful use of the model(s) are:

- First, information for the variables identified in the equations selected above should be made available by the firm/farm at the time of processing or immediately prior to processing of the birds. These data should be collected and presented on standardized data



collection forms.

- Second, the veterinarian must take the data for the variables selected and generate a predicted value for  $X_{109}$  which is the disease rate for the particular flock to be processed.
- Finally, using the  $X_{109}$  value computed above, the veterinarian calculates a predicted value of  $Y_2$ , the condemnation rate expected for the particular flock. The computation of  $X_{109}$  and  $Y_2$  could be handled in one of two ways.

6.5.1. Alternative 1 - Using hand calculators-This approach is rather simple and straight forward. The veterinarian only requires preexisting information on the predictor variables. The coefficients of these  $X_k$  variables is known from the model and once their values are provided, one then computes either  $X_{109}$  or  $Y_2$  directly using a hand calculator. With the availability of various hand calculators, such computations should be accomplished with ease.

6.5.2. Alternative 2 - Using microcomputers-The manipulation of data for scientific computations and/or for record keeping are nowadays handled easily with the aid of microcomputers. Information processing which includes the storage, analysis and display of information needed for decision making by individual, or organizations such as in poultry carcass inspection may have to now rely on the use of computers. In the case of poultry, it is obvious that

a large amount of data is being generated by the poultry industry and the Food Safety and Inspection Service (FSIS). Most of these data may best be stored and retrieved for various decision making tasks. In the case at hand, a predictor model has been developed which relies on the availability of data for selected variables. To facilitate this, a program could be prepared so as to enable:

- the coding and storage of relevant poultry related data on a computer,
- the analysis of the data including computations of predicted  $\hat{Y}_2$  values using the predictor models developed.

Based on current information, the veterinarian could then easily interact with a microcomputer and obtain a set of instructions to facilitate the decision making task for the type of inspection best suited to individual flocks. Such a computer program could be prepared in the form of a menu where one peruses available alternatives and responds to those questions until the terminal objective has been achieved.

Additionally, via such microcomputers located in the various poultry processing plants throughout the country, FSIS could maintain a network of information gathering devices with connections to a central data base in some specified place. Since such a data base is inherently rich and quite accurate and reliable in the case of

poultry, FSIS may be in a position, not only to use micro-computers for implementing the models developed in this project in the field, but it would also be in an enviable position of utilizing its data base for various tasks with potential benefit to the poultry industry as well as to FSIS. Therefore, it is felt that one of the best alternatives for implementing the use of the predictor models developed here in the field could be via the introduction of microcomputers to facilitate data handling and decision making in poultry inspection. This would be of great benefit to the poultry industry, and to the veterinary profession itself, whereby, for example, some of the expertise of veterinarians and poultry inspectors may be diverted to expand the utilization of current information technology in their respective areas.

## 7. RECOMMENDATIONS

### 7.1. Which model to use for prediction:

For predictive purposes, the best predictor model to use for predicting  $Y_2$ :

$$\hat{Y}_2 = 19.3453 - 0.21023X_{63} - 0.10355X_{14} + 0.20511X_{109} + 0.3227X_{129} - 0.43571X_{205} - 0.00702X_{223} + 0.18366Y_{2T}$$

For predicting disease specific condemnation rate

( $Y_{14}$ ):

$$\hat{Y}_{14} = 0.21854 + 0.02816X_{61} - 0.000534X_{84} + 0.13305X_8 - 0.0000606X_{19} + 0.02748X_{88} + 0.00451X_{109} - 0.00153X_{148} - 0.01245X_{205} - 0.03942X_{208}$$

For predicting the disease rate for the flock ( $X_{109}$ ):

$$\hat{X}_{109} = 27.61194 - 0.37163X_{63} + 0.1091X_{148} + 0.36292X_{133}$$

or

$$\begin{aligned}\hat{X}_{109} = & 39.54751 - 2.91267X_{58} - 2.02945X_{261} - 0.44252X_{65} \\ & + 3.23479X_{27} - 0.55159X_{39} + 1.9965X_{117} + 1.57413X_{169} \\ & + 1.04076X_{189} - 1.8702X_{208} - 1.92553Z_6 + 9.36482T_{pop}\end{aligned}$$

## 7.2. The model for classification purposes:

For classifying a given flock into high or low condemnation groups, the best discriminant models for arbitrarily set demarcation points for condemnation rates have been provided under discriminant models. Those equations were very good in providing decision making information at the indicated levels which varied from 0.1% to 5%.

## 7.3. How to use the models:

This had been described above under the various sections. However, in summary form, in order to use the models developed herein, the steps required are:

- collect data for the selected variables identified by the model using standardized data collection forms. This way, each farm would be collecting and providing FSIS with records which would be comparable and hopefully reliable. Such records should be made available to the inspector in charge before the birds from a given farm were to be processed.
- using these records, the inspector in charge will first compute a predicted value for the estimated disease rate ( $\hat{X}_{109}$ ) in the given flock of birds.

- then, the value for  $X_{109}$  and the other selected variable data are utilized to compute a predicted value for  $Y_2$  or  $Y_{14}$ , the average condemnation rate due to diseases or the disease specific condemnation rate referred to as the others category. In a similar manner, values for low condemnation rate (LC) or high condemnation rate (HC) are computed to facilitate the classification of flocks into high or low categories.
- based on the value of  $Y_2$ , LC or HC, a decision will be made by the inspector using guidelines set up by FSIS as to where to draw the line between a (predicted) condemnation rate which may require "scaled down" inspection vs another alternative.

#### 7.4. Areas for further studies in the future:

The work involved in this project, overwhelming as it was, has opened up numerous areas for which further studies are required. The results from such studies will be useful in future decision making in poultry inspection. A few of the major areas for such a follow up are briefly presented below.

##### 7.4.1. Independent validation of the model developed in this project in different regions of the U.S.:

To test and verify the predictive value of the model, it is essential that it be utilized in the field in different regions of the U.S. on a pilot study basis. Only then could its validity be established before wider applications as an adjunct to existing poultry inspection



procedures are carried out. The pilot validation test implementation could involve randomly selecting a few processing plants in the country and then testing the results under those situations over a period of a few months to a year. Based on the performance of the model under these circumstances, a final decision could be made on its utility in future endeavours.

7.4.2. Conducting comparable types of studies, as conducted in this project, in other regions of the U.S. - This is another option which could be beneficial in the long run. This point becomes significant in the sense that, rather than one general model which could be applied uniformly across the country, the preferable option may be to develop models which could be useful on a regional basis. Additionally, due to passage of time, the diseases of importance in current poultry condemnation or their determinants, whether on a national or regional basis, may change and therefore, the predictive models in use will have to be reevaluated and adjusted to accommodate such changes.

7.4.3. Condemnation of parts of poultry carcass due to diseases - This aspect of poultry condemnation, no doubt, will be an area which urgently needs further studies. Currently, it is not required by FSIS, to record separately from other causes, the parts condemned due to diseases. Yet, a sizeable amount of inspection time is spent on determining which part(s) are to be trimmed by plant personnel. Both

of these tasks are not only time consuming, but also complex. There are numerous disease conditions that require trimming. To name a few, gangrenous dermatitis, hemorrhagic syndrome, scabby hip syndrome, staphylococci infection, and fowl pox. When whole bird condemnation due to disease decreases substantially, parts condemned may then become the important contributor to economic loss. Therefore, accurately recording the trimming due to different reasons will benefit the processors to correct these problems.

7.4.4. Revision of recording method and terminology. The MPI form 514-1 (Poultry Condemnation Certificate) should be updated. For example, tuberculosis is no longer a common disease encountered in poultry processing plants. Therefore, this item should be deleted from the form. Numerous disease conditions which result in condemnation of parts of the bird are not recorded at the present time and should be added to the form.

7.4.5. Serological profile studies - Although the value of serological profile as a predictor for condemnation has not been shown, there is a need to conduct more studies before its importance can be established. There are many factors affecting serological profiles. The limited resources and time spent in serological tests in this project, by no means were adequate to examine the validity of this factor. There are several disease agents proven to be directly or indirectly associated with

airsacculitis. They are MS, MG, Newcastle disease virus, infectious bronchitis, infectious bursal disease and perhaps adenovirus. Among these agents, commercial flocks are routinely vaccinated with Newcastle disease and infectious bronchitis virus. An average vaccination titer of normal birds at a specific age should be predetermined before a diagnosis of disease condition can be made, (although in a disease condition the serum titer is usually higher). In order to thoroughly study the serological profile of a flock, antibodies against MG, MS, Newcastle disease, infectious bronchitis and infectious bursal disease should be monitored throughout the life of the flock, instead of testing only at 4 and 7 weeks of age. An increase in HI titer for Newcastle disease and virus neutralization titer in the sera of broilers about 10 days before processing, may indicate a condition of active infection in the last few days, as a result of the infection, condemnation due to airsacculitis may increase since airsacculitis is believed to be related to ND and IB. However, the relationship of serologic titer with the rate of condemnation has to be determined before one can speculate its importance in predicting the rate of condemnation. To the investigators of this project, this factor (serologic titer) may still have potential in predicting condemnation.

- 7.4.6. Microbiological profile - Bacterial and fungal flora in hatcheries and poultry houses were studied in very few

flocks. Since the presence of large numbers of E. coli, Pasteurella multocida and Aspergillus fumigatus will influence the incidence of airsacculitis, more studies concerning the bacterial and fungal flora in their environment are needed before definitive conclusions can be made.

- 7.4.7. Specific guidelines for condemnation of septicemia and toxemia are needed - Septicemia and toxemia are conditions developed in animals as a result of infections caused by different agents. The clinical manifestations are different, and guidelines for diagnosis are poorly defined.

Birds condemned for septicemia-toxemia have become the single biggest category of economic loss for poultry companies. Apparently, due to ambiguous criteria for this disease condition, sometimes instead of condemning part of the bird, the entire carcass had to be condemned, simply because the bird "looked septicemic". Therefore more clear cut guidelines for this condition is urgently needed. However, before the new guidelines can be established, research concerning the true picture of septicemia-toxemia in terms of signs and symptoms, and whether the meat from birds showing signs of septicemia and toxemia were detrimental to animal and human health, must be established. may be possible to salvage part of or the entire bird, provided that clear cut guidelines are established.

In recent years, condemnation due to this category

has increased, the increase may have been the results of mild forms of disease conditions such as ND and IB, or adverse effects of vaccination. There are several emerging disease conditions which have been reported in recent years, e.g. malabsorption syndrome, pale bird syndrome, brittle bone disease, proventriculus adenovirus infections. In addition, infectious bursal disease has become wide spread in all parts of this country; and early infection of this disease in baby chicks resulted in immunosuppression, and many emaciated birds. All these disease conditions could result in increased condemnation rate in the septicemia and toxemia category. Therefore, more research is needed in this area in the near future.

- 7.4.8 Others - It was consistently demonstrated in this study that there is a close relationship between weather, ventilation, strain of birds, number of strains of birds, medication records, different vaccines used and condemnation rate. It is the authors opinion that long term studies concerning these aspects of poultry health should be initiated.

The relationship of feed consumption and feed conversion to condemnation has not been established, due to the fact that there is no accurate method for measuring the weekly or daily feed consumption. However, accurate measures of feed consumption during a given period will be helpful for future analysis.



#### 7.5. Concluding Remarks

Finally, it is significant to reemphasize here that analytic models which interrelate such biological and mathematical complexities are relatively new in veterinary medicine and are now receiving long overdue attention (68, 69, 75, 76). It is encouraging and pleasing that FSIS had the foresight to consider such an alternative to poultry inspection which provided us an opportunity to explore extensively, the utility of such holistic approaches to problem solving in an industry where population health data is relatively valid and well maintained.

The future for the application of systems analysis and the development of computer models to facilitate decision-making tasks in veterinary medicine appears bright; this project was one such example. At a time when information processing is crucial to decision-making, more areas of veterinary health care would have to be managed with the aid of computers. The inspection of poultry products appears to be one such area where an introduction of computer aided decision-making models could be of great value. Although, this project was but a beginning in such a direction, further research and testing of results will be essential before the full benefits of such problem solving tools could be realized.

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Form 1

## APPENDIX 1

Form CodePOULTRY DISEASE RESEARCH

School of Veterinary Medicine  
Tuskegee Institute

Flock Testing Feasibility StudyCODE/COL.Cross-Sectional Sampling - Farm Data

NOTE: The farm data should be followed up by corresponding data from processing plant.

Date (mo/dy/yr) \_\_\_\_\_ Visit No. (1,2,3,4) \_\_\_\_\_

Data collected by (Code) \_\_\_\_\_

County \_\_\_\_\_

Firm Code \_\_\_\_\_ No. of growers of this firm \_\_\_\_\_

Farm Code \_\_\_\_\_ Brood No. (1,2,3,4,5) \_\_\_\_\_

Distance to nearest poultry farm (miles) \_\_\_\_\_

X1

X2

A. Population Data For Farm:

1. Total number of birds (1st week) \_\_\_\_\_

X3

2. Age of birds (days) \_\_\_\_\_

X4

3. Average weight of birds at this age (lbs) \_\_\_\_\_

X5

4. Are birds of this age group of uniform size?

X6

1 yes \_\_\_\_\_

0 no \_\_\_\_\_

5. If not, estimate proportion of undersized birds (%) \_\_\_\_\_

X7

6. Major strain of birds:

1. Strain group 1 \_\_\_\_\_

X8

2. Strain group 2 \_\_\_\_\_

X9

3. Strain group 3 \_\_\_\_\_

X10

4. Strain group 4 \_\_\_\_\_

Z1

7. Breeder Flock sources

1. Breeder source 1 \_\_\_\_\_

X11

2. Breeder source 2 \_\_\_\_\_

X12

3. Breeder source 3 \_\_\_\_\_

X13

4. Breeder source 4 \_\_\_\_\_

Z2

8. Strain/breeder follow-up:

<u>House Id</u>	<u>No. of Birds</u>	<u>Strain Type</u>	<u>Breeder Flock</u>
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
Totals	_____	_____	_____

				CODE/COL.
9.	Total number of strains on farm _____			X14
10.	Total number of breeder flock sources for farm _____			X15
11.	Housing:			
	1.	House type 1 (conventional/fan) _____		X16
	2.	House type 2 (conventional/no fan) _____		X17
	3.	House type 3 (others) _____		Z3
12.	House type follow-up:			
	House Id	Type of House	Area of House (sq. ft.)	Total Birds in House
	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____
	Totals	_____	_____	_____
**				
13.	Average population density per square feet _____			X18
14.	Average distance between houses on farm (ft.) _____			X19
15.	Type of ventilators:			
	1.	Type 1 (3 CFM) _____		X20
	2.	Type 2 (5 CFM) _____		X21
	3.	Type 3 (Others) _____		Z4
16.	Number of ventilators (Total for all houses) _____			X22
17.	Location of intakes: (geographic direction)			
	1.	Roof _____		X256
	2.	East, north east _____		X23
	3.	North, north west _____		X24
	4.	West, south west _____		X25
	5.	South, south east _____		Z5
18.	Location of exhausts: (geographic direction)			
	1.	Roof _____		X257
	2.	East, north east _____		X26
	3.	North, north west _____		X27
	4.	West, south west _____		X28
	5.	South, south east _____		Z6

## B. Morbidity/Mortality data from farm records

				CODE/COL.
1.	By housing:	No. of birds sick	No. of birds	Total No.
	<u>House Id.</u>	<u>so far</u>	<u>dead so far</u>	<u>birds in</u>
				<u>house</u>
	Totals			
**	2.	Farm morbidity rate (prevalence)		X29
**	3.	Farm mortality rate		X30
**	4.	House type specific mortality rates:		
		House type 1		X31
		House type 2		X32
		House type 3		X33
		House type 4		X258
**	5.	House type specific morbidity rates:		
		House type 1		X34
		House type 2		X35
		House type 3		X36
		House type 4		X259
6.	By age (week)	Estimated % sick	No. of birds	Total No.
			dead	of birds
				on farm
	1st			
	2nd			
	3rd			
	4th			
	5th			
	6th			
	7th			

\*\* Denotes values computed.



				CODE/COL.
** 7. Age specific morbidity rates:				
1. end of week 4 _____				X37
2. end of week 7 _____				X38
** 8. Age specific mortality rates:				
1. end of week 4 _____				X39
2. end of week 7 _____				X40
9. Major causes of morbidity (diseases) on farm based on farm records (top 5 diseases at end of 7 weeks):				
House Id.	Diseases (Infection)	No. affected	List of Diseases	
_____	_____	_____	1. Leukosis	
_____	_____	_____	2. Septicemia	
_____	_____	_____	3. Airsacculitis	
_____	_____	_____	4. Synovitis	
_____	_____	_____	5. Tumors	
_____	_____	_____	6. Others	
** 10. Disease specific morbidity rates for farm:				
1. _____				X41
2. _____				X42
3. _____				X43
4. _____				X44
5. _____				X45
6. _____				X46
11. Estimated (recorded) incidence of diseases on farm (%) _____				X47
12. Estimated (recorded) prevalence of diseases on farm (%) _____				X48

\*\* Denotes values computed.

13. Major causes of mortality on farm based on necropsy records of farm:

House Id.	Disease (at Necropsy)	No. Affected	List of diseases
_____	_____	_____	1. Leukosis
_____	_____	_____	2. Septicemia
_____	_____	_____	3. Airsacculitis
_____	_____	_____	4. Synovitis
_____	_____	_____	5. Tumors
_____	_____	_____	6. Others

\*\*

14. Disease specific mortality rates from farm necropsy records (%):

1	_____	X49
2	_____	X50
3	_____	X51
4	_____	X52
5	_____	X53
6	_____	X54

15. Estimated (recorded) mortality rate on farm (%)  
(4 weeks) \_\_\_\_\_

X55

16. Estimated (recorded) mortality rate on farm (%)  
(7 weeks) \_\_\_\_\_

X56

C. Hatch Data:

1. Hatchery source for this brood

1. Hatchery Source 1	_____	X57
2. Hatchery Source 2	_____	X58
3. Hatchery Source 3	_____	X59
4. Hatchery Source 4	_____	X260
5. Hatchery Source 5	_____	X261
6. Hatchery Source 6	_____	X262
7. Hatchery Source 7	_____	X263
8. Hatchery Source 8	_____	Z7

				CODE/COL.
2. Type of incubators:				
Incubator type 1		_____		X60
Incubator type 2		_____		X61
Incubator type 3		_____		Z8
3. Distance from hatchery to farm _____				X268
4. Average fertility rate for hatchery _____				X62
Week (Age)	Breeder Flock	Fertility Rate (%)	Hatchability Rate (%)	
_____	_____	_____	_____	
_____	_____	_____	_____	
_____	_____	_____	_____	
_____	_____	_____	_____	
_____	_____	_____	_____	
_____	_____	_____	_____	
_____	_____	_____	_____	
5. Average hatchability rate for hatchery (%) _____				X63
6. Average fertility rate for this brood of birds (%) _____				X64
7. Average hatchability rate for this brood of birds (%) _____				X65
8. Number of days eggs held on farm _____				X66
9. Number of days eggs held in hatchery _____				X67
10. Are eggs from more than one flock hatched simultaneously in same hatchery?				X68
1    yes _____				
0    no    _____				
11. Number of breeder flocks supplying eggs for hatchery _____				X69
12. Average temperature (F) for holding eggs (farm) _____				X70
13. Average temperature (F) for holding in hatchery _____				X71
14. Average temperature (F) in hatchery _____				X72
15. Average relative humidity in hatchery (%) _____				X73
16. Sanitation assessment for hatchery area: (where 1 = good, 2 = satisfactory, 3 = poor)				
Criteria		Grade (1, 2, 3)		
1. Offensive odor (unspecified source)		_____		
2. Dusty room (and equipment)		_____		
3. Cobwebs on walls/ ceilings		_____		
4. Freedom from garbage and refuse		_____		
5. Waste disposal containers availability		_____		
6. Unwashed (unsanitary) equipment/areas		_____		

		CODE/COL.
**	17. Hatchery sanitation index (average of grades for criteria 1-6) _____	X74
18. Type of ventilators:		
1.	Ventilator type 1 (3 CFM) _____	X75
2.	Ventilator type 2 (5 CFM) _____	X76
3.	Ventilator type 3 (Others) _____	Z9
19.	Number of ventilators _____	X77
20. Location of intakes (direction):		
1.	Roof _____	X264
2.	East, north east _____	X78
3.	North, north west _____	X79
4.	West, south west _____	X80
5.	South, south east _____	Z10
21. Location of exhausts (direction):		
1.	Roof _____	X265
2.	East, north east _____	X81
3.	North, north west _____	X82
4.	West, south west _____	X83
5.	South, south east _____	Z11
D. Brooding Data:		
1.	Date of setting of eggs for this brood (mo/dy/yr) _____	X84
2.	Date of placing of chicks for this brood (mo/dy/yr) _____	X85
3.	Number of chicks dead or arrival _____	X86
4.	Length of time for preheating (brooder) (hrs) _____	X87
5.	Brooding:	X88
	1 Whole _____	
	0 Partial _____	
6.	Length of stay of birds in broiler house (days) _____	X89
7.	Age when brooder guards are removed (days) _____	X90
8.	Number of chicks per broiler house (average) _____	X91
9.	Square footage per bird per broiler house _____	X92
10.	Microclimate (Average temperature/humidity) in broiler house (if available)	
Week	Average Temp. (F)	Average Relative Humidity (%)
1st	_____	_____
2nd	_____	_____
3rd	_____	_____
4th	_____	_____
5th	_____	_____
6th	_____	_____
7th	_____	_____

	CODE/COL.
** 11. Average temperature (F) up to 4th week _____	X93
** 12. Average temperature (F) end of 7th week _____	X94
** 13. Average relative humidity up to 4th week (%) _____	X95
** 14. Average relative humidity end of 7th week (%) _____	X96

E. Serologic Profile: (Laboratory)

1. Indicator Disease	Age of Birds	No. of Samples Examined	No. of Pos.
ND	4 wks	_____	_____
MYC	4 wks	_____	_____
ND	7 wks	_____	_____
MYC	7 wks	_____	_____
_____	_____	_____	_____

** 2. Average infection rate based on serological tests (%)	
1. at 4 weeks _____	X97
2. at 7 weeks _____	X98

## 3. Commercial serological data:

Date of Testing (mo/dy/yr)	Age Tested (days)	Serological Tests Performed (Type)	Total Samples Tested	No. of Pos.
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____

4. Average infection rate based on commercial tests (%) _____	X99
---	-----

F. Microbiological Profile: (at 4 weeks of age)

1. Location Sampled	Population estimate	
Hatchery Room	_____	X100
Brooder House	_____	X101
2. Number of microbial colonies counted: (Average)		
	Hatchery	Brooder House
1. Media 1 (Blood base)	_____	_____
2. Media 2 (McKonkeys)	_____	_____
3. Media 3 (Cornmeal)	_____	_____
		X102

\*\* Denotes values computed.



## 4. Major types of genera identified:

	<u>Hatchery</u>	<u>Brooder House</u>	CODE/COL.
1. Genus			X104
2. Genus			X105
3. Genus			X106
4. Genus			X107
5. Genus			X103

G. Necropsy Profile (Laboratory):

1. Age at Necropsy	Total No. of Birds Necropsied	Total No. of Birds Diseased (grossly)
4 wks		
7 wks		

\*\*

## 2. Average disease rate based on laboratory (necropsy) (%)

1. at 4 weeks		X108
2. at 7 weeks		X109

## 3. Top 5 common diseases diagnosed (Laboratory):

Total No. Birds Necropsied	Diagnoses (disease)	No. Diagnosed	List of Diseases
			1. Leukosis
			2. Septicemia
			3. Airsacculitis
			4. Synovitis
			5. Tumors
			6. Others

\*\*

## 4. Disease specific rates based on necropsy (laboratory):

1.		X110
2.		X111
3.		X112
4.		X113
5.		X114
6.		X115

Week	No. of Birds Medicated	No. of Birds Became Sick	No. of Birds Dead
1st			
2nd			
3rd			
4th			
5th			
6th			
7th			

\*\*Denotes values computed.

H. Feed Consumption/Utilization Data:

				CODE/COL.
1.	Type of feed used			
	1. Mash _____			X116
	2. Crumbles _____			X117
	3. Pellets _____			Z12
2.	Feeding schedule (times per day)			Z118
	1 ad lib _____			
	0 at intervals _____			
3.	Feeder space per bird _____			X119
4.	Location of feeders during brooding (height in in.) _____			X120
5.	Feed spillage on ground:			X121
	1 Yes			
	0 No			
6.	Feed source (company): (is same as firm) A,B,D			
	1. Source 1 ( ) _____			X122
	2. Source 2 ( ) _____			X123
	3. Source 3 ( ) _____			X124
	4. Source 4 ( ) _____			X266
	5. Source 5 ( ) _____			Z13
7.	How often is feed delivered? (per month) _____			X125
8.	Last date of feed delivery (mo/dy/yr) _____			X126
9.	Number of waterers used during brooding _____			X127
10.	Type of waterers			X128
	1 manual _____			
	0 automatic _____			
11.	Water spacing per bird _____			X129
12.	Age manual waterers removed _____			X130
13.	Water spillage on ground			X131
	1 Yes _____			
	0 No _____			
14.	Feed utilization by farm:			
	House Id.	No. of Birds	Feed Consumed/ Week/house	Estimated Weight Gain/visit
	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____

					CODE/COL.
** 2. Estimated efficiency rate for prophylactics (%):					
1. End of 4 weeks _____					X138
2. End of 7 weeks _____					X139
3. Route of prophylactic medications:					
1 via feed _____					X140
2 via water _____					X141
3 via aerosol _____					X142
4 others _____					Z14
4. Type of prophylactic medications:					
1 antibiotics _____					X143
2 anticoccidials _____					X144
3 others _____					Z15
5. Types of specific diseases prophylactics applied for:					
1 Bacterial _____					X145
2 Viral _____					X146
3 Parasitic _____					X147
4 Others _____					Z16
6. Average duration (length of prophylactic medications) (days) _____					X148
7. Dosages of prophylactic medications are based upon:					
1. per ton of feed _____					X149
2. number of birds _____					X150
3. other guidelines _____					Z17
8. Therapeutic drug use:					
Week	No. of Birds Sick	No. of Birds Treated	No. of Birds Recovered	No. Birds Dead	
1st	_____	_____	_____	_____	
2nd	_____	_____	_____	_____	
3rd	_____	_____	_____	_____	
4th	_____	_____	_____	_____	
5th	_____	_____	_____	_____	
6th	_____	_____	_____	_____	
7th	_____	_____	_____	_____	

	CODE/COL.
** 9. Estimated efficiency rate for therapeutics (%)	
1. End of 4 weeks _____	X151
2. End of 7 weeks _____	X152
10. Types of diseases therapy applied for:	
1 Bacterial _____	X153
2 Viral _____	X154
3 Parasitic _____	X155
4 Others _____	No code
11. Types of therapeutic drugs used:	
1 Antibiotics _____	X156
2 Sulfas _____	X157
3 Others _____	No code
12. Routes of therapy:	
1 via feed _____	X158
2 via water _____	X159
3 via aerosol _____	X160
4 Others _____	No code
13. Dosages based upon:	
1 Number of birds _____	X161
2 Per ton of feed _____	X162
3 Others _____	No code
14. Average length of therapy (days) _____	X163
15. Feed additives and growth promoters:	
1 feed additives only _____	X164
2 growth promoters only _____	X165
3 no additives _____	Z18
16. Source company for additives and growth promoters	
1 Company _____	X166
2 Company _____	X167
3 Company _____	X168
4 Others _____	No code



J. Vaccination Data:

CODE/COL.

1. Manufacturer(s) of vaccine:

<u>Vaccine</u>	<u>Manufactuter</u>	<u>Names of Manufactuters</u>
_____	_____	1. Vineland
_____	_____	2. Sterwin
_____	_____	3. Salisbury
_____	_____	4. Others

X169

X170

X171

Z19

2. Routes of vaccinations:

- 1 oral \_\_\_\_\_
- 2 injections \_\_\_\_\_
- 3 others \_\_\_\_\_

X172

X173

Z20

3. Schedule of vaccination:

<u>Time</u> <u>(Week)</u>	<u>Vaccine</u> <u>given (used)</u>	<u>Type (1=live virus,</u> <u>2=attenuated, 3=</u> <u>killed product)</u>	<u>List of Vaccines</u>
1st	_____	_____	1. Marek's Dis.
2nd	_____	_____	2. Newcastle
3rd	_____	_____	3. Bronchitis-Inf.
4th	_____	_____	4. Gumboro (inf. bursal)
5th	_____	_____	5. Laryngotrachei- tis-Inf.
6th	_____	_____	6. Fowl pox
7th	_____	_____	7. Others

4. Vaccines given before 4 weeks of age:

1. Vaccine \_\_\_\_\_
2. Vaccine \_\_\_\_\_
3. Vaccine \_\_\_\_\_
4. Vaccine \_\_\_\_\_

X174

X175

X176

Z21

5. Vaccines given after 4 weeks of age:

1. Vaccine \_\_\_\_\_
2. Vaccine \_\_\_\_\_
3. Vaccine \_\_\_\_\_
4. Vaccine \_\_\_\_\_

X177

X178

X179

No Code

6. Number of repeated vaccinations \_\_\_\_\_

X180

7. Type of vaccine(s) given:	CODE/COL.
1. Killed product _____	X181
2. Live virus _____	X182
3. Attenuated _____	Z22
8. Previous types of vaccines used on farm:	
1. same as above _____	X183
0 not same as above _____	
9. Number of birds showing reaction to vaccine _____	X184
10. Severity of reaction:	X185
1 severe _____	
2 moderate _____	
3 slight _____	
K. <u>Sanitation Indicators:</u>	
1. Assessment of broiler farm sanitation (where grade of 1=good, 2=satisfactory, 3=poor)	
<u>Criteria</u>	<u>Grade (1,2,3)</u>
1. Offensive odor (unspecified source) _____	
2. Dusty room (and equipment) _____	
3. Cobwebs on wall/ceilings _____	
4. Freedom from garbage and refuse _____	
5. Waste disposal containers availability _____	
6. Unwashed (unsanitary) equipment/areas _____	
2. Farm sanitation index (average of grades for criteria 1-6) _____	X186
3. How are dead birds disposed of?	
1 pit _____	X187
2 incinerated _____	X188
3 others _____	Z23
4. Type of litter used?	X189
1 shavings _____	
2 peanut hull _____	X267
3 sawdust _____	Z24

	CODE/COL.			
5. Depth of litter (estimate) (inches) _____	X190			
6. How often is the litter changes? _____	X191			
7. Is the litter changed: 1 partially _____ 0 completely _____	X192			
8. How is the litter removed: 1 tractors _____ 0 others _____	X193			
9. How many batches in this litter? _____	X194			
10. Procedure for house cleaning after litter is removed? 1 remove litter _____ 2 wash floor _____ 3 disinfect floor _____ 4 not any of above _____	X195 X196 X197 No code			
<b>L. Health Care Data:</b>				
1. Cost of medication (\$ per brood) _____	X198			
2. Cost of vaccination (\$ per brood) _____	X199			
3. Number of times a veterinarian visited farm to provide health care for this brood _____	X200			
4. Total number of hours veterinarian spent on farm for this brood _____	X201			
<b>M. Macroclimatic Data:</b>				
1. County weather station where farm located _____				
2. Summary macroclimatic data at (two week) intervals:				
Dates (mo/dy/yr)	Avg. max. temp. (F)	Avg. temp. (F)	Avg. min. temp. (F)	Total Preci- pitation (in)
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
_____	_____	_____	_____	_____
3. Average maximum temperature (F) _____	X202			
4. Average temperature (F) _____	X203			

5. Average minimum temperature (F) _____	CODE/COL. X204
6. Average total precipitation _____	X205
7. Number of rainy days _____	ZR
8. Season during which this brood of birds was raised:	
1. fall _____	X206
2. winter _____	X207
3. spring _____	X208
4. Summer _____	Z25

Supplement:

Management Indicators: (Below, a grade of 1=good, 2=satisfactory, and 3=poor)

## 1. Assessment of farm record keeping:

<u>Criteria</u>	<u>Grade (1,2,3)</u>
1. Records well organized _____	
2. Records easily retrievable _____	
3. 75% of information easily available (grade=1) _____	
4. 50%-75% of information easily available (grade=2) _____	
5. Less than 50% of information found (grade=3)	

2. Record keeping _____	X209
-------------------------	------

3. Are records kept in a secure place?	X210
--	------

1 yes \_\_\_\_\_

0 no \_\_\_\_\_

## 4. Cooperative attitude of farm personnel:

<u>Criteria</u>	<u>Grade (1,2,3,)</u>
1. Answer questions courteously _____	
2. Volunteer information _____	
3. Provide assistance when asked _____	

5. Index of cooperation (average) _____	X211
---	------

## 6. Assessment of farm (organization) and management:

Criteria	Grade (1, 2, 3)	CODE/COL.
1. Grade for recording keeping _____		
2. Grade for cooperation _____		
3. Grade for sanitation _____		
4. Others (if any) _____		
7. Average grade for farm management _____		X212
8. Security - Is there a disease surveillance program on this farm?		X213
1 yes _____		
0 no _____		
If yes, explain briefly _____		
_____		
_____		
9. Security - Is there an emergency plan to deal with a disease outbreak on this farm:		X214
1 yes _____		
0 no _____		
If yes, explain briefly _____		
_____		
_____		
10. Physical security of farm - Is there a program to prevent theft and other related problems		X215
1 yes _____		
0 no _____		
11. Are there safety and other warning signs for employees to prevent accidents, zoonotic infections, etc.?		X216
1 yes _____		
0 no _____		
12. Rodent control program used:		
1. Traps _____		X217
2. Poisons _____		X218
3. No program _____		No code



	CODE/COL.
13. If a rodent control program exists, how would the farmer rate its success?	
1. successful _____	
2. partially successful _____	
3. not successful _____	
14. Other management indicators which may be pertinent _____	X219
_____	
_____	
_____	
_____	

X220

Poultry Disease Research

School of Veterinary Medicine

Tuskegee Institute

Flock Testing Feasibility Study

## II. Cross-Sectional Sampling - Processing Plant Data

NOTE: Date should be collected from birds for which farm data has already been obtained

Date (mo/dy/yr) \_\_\_\_\_ Visit No. (1,2,3,4) \_\_\_\_\_

Data collected by (code) \_\_\_\_\_

Processing Plant Code \_\_\_\_\_ Location (city/county) \_\_\_\_\_

Firm Code \_\_\_\_\_

Source Farm code \_\_\_\_\_

Distance from Tuskegee (miles) \_\_\_\_\_

## A. Pre-Processing Data:

1. Number of birds shipped from farm for processing \_\_\_\_\_ X221

2. Average slaughter weight on date of marketing (lbs) \_\_\_\_\_ X222

3. Distance from farm to plant (miles) \_\_\_\_\_ X223

4. Number of hours of driving from farm to processing plant \_\_\_\_\_ X224

5. Trucks and crews owned by plant? \_\_\_\_\_ X225

1 yes \_\_\_\_\_

2 no \_\_\_\_\_

6. Number of different drivers involved in flock delivery \_\_\_\_\_ X226

7. Number of trips to haul the whole flock to the plant \_\_\_\_\_ X227

8. Number of trucks used to transport birds \_\_\_\_\_ X228

9. Type of coops used to transport birds \_\_\_\_\_ X229

1 wooden frame \_\_\_\_\_ X266

2 plastic \_\_\_\_\_ X225

3 steel \_\_\_\_\_ X230

CODE/COL

## APPENDIX 2

	CODE/COL
10. Approximate number of birds per coop (cage) _____	X230
11. Approximate number of birds per truck _____	X231
12. Estimate time of day when birds from the farm were processed and inspected _____	X233
13. Method of cooling birds in transit: 1 fans _____ 0 others _____	
14. Method of cooling birds at processing plant: _____ 1 fans _____ 0 others _____	X234
15. Number of birds dead on arrival at plant _____	X235
16. Total number of birds slaughtered _____	X236
17. Number of days involved in marketing this flock (from first to last bird to leave the farm) _____	X237
B. <u>Macroclimate data on date of processing:</u>	
1. <u>Average temperature (F) for the day</u> _____	X238
2. <u>Was it rainy or dry (rainy=1, dry=0)</u> _____	X239
3. <u>Average relative humidity (%) for the day</u> _____	X240
C. <u>Inspection</u>	
1. Number of inspectors on line _____	X241
2. Number of veterinarians(s) in plant _____	X242
3. Line speed (average per day) per min. _____	X243
4. Type of inspection: 1. hands off _____ 2. semi-traditional _____ 3. traditional _____ 4. others _____	
D. <u>Processing Plant:</u>	
1. processing plant No. 1 (A) _____	X247
processing plant No. 2 (B) _____	X248
processing plant No. 3 (D) _____	X249
processing plant No. 4 (E) _____	X250
processing plant No. 5 (F) _____	

	CODE/COL
2. Daily total capacity of processing plant _____	X251
3. Number processed this day _____	X252
4. Total number of employees in plant _____	X253
5. Number of hours per day that plant operates _____	X254
6. Number of shifts _____	X255

E. Condemnation data:

1A. Condemnation due to diseases for specific farms on this day:

Farm ID	No. inspected and passed	No. condemned (whole carcass)	Cause of Con- demnations	Lbs. trimmed due to diseases
Study	_____	_____	_____	_____
farm	_____	_____	_____	_____
	_____	_____	_____	_____
	_____	_____	_____	_____
Totals	_____	_____	_____	_____
All Farms A	_____	_____	_____	_____
	_____	_____	_____	_____
B	_____	_____	_____	_____
C	_____	_____	_____	_____
D	_____	_____	_____	_____
E	_____	_____	_____	_____
Totals	_____	_____	_____	_____
All Farms A	_____	_____	* * *	Y19
B	_____	_____	* * *	Y20
C	_____	_____	* * *	Y21
D	_____	_____	* * *	Y22
E	_____	_____	* * *	Y23
Grand	_____	_____	_____	_____
Total	_____	_____	_____	_____

		CODE/COL
**	2. Average condemnation rate due to diseases for processing plant (this day) (whole carcass)_____	Y1
**	3. Condemnation rate due to diseases for study farm (whole carcass)_____	Y2
**	4. Disease specific condemnation rates for all farms (whole carcass)	
		Y3
		Y4
		Y5
		Y6
		Y7
		Y8
** denotes values to be computed		
**	5. Disease specific condemnation rates for study farm (whole carcass)	
		Y9
		Y10
		Y11
		Y12
		Y13
**		Y14
**	6. Overall condemnation rate due to diseases for study farm (whole carcass + trimmed parts)_____	Y15



## 7. Non-disease condemnations:

Farm ID	No. condemned (whole carcass)	Lbs. of parts condemned (trimmed) (lbs)	Cause of Condem- nations
Study			
Farm			
Totals			
All Farm 1A			
B			
C			
D			
E			
Totals			
Grand Totals			

\*\* Denotes values to be computed

- e. How often are condemned birds disposed? \_\_\_\_\_
- f. Method of disposal \_\_\_\_\_
- g. Do birds fall onto the floor?
- 1 yes often \_\_\_\_\_
- 2 occassionally \_\_\_\_\_
- 3 none \_\_\_\_\_

\*\* denotes values to be computed

	CODE/COL
** 8. Average condemnation rate due to non-diseases for processing processing plant (this day) (whole carcass)_____	Y16
** 9. Condemnation rate due to non-diseases for study farm (whole carcass)_____	Y17
** 10. Overall condemnation rate (whole carcass + parts trimmed) due to non-disease cause_____	Y18

F. Miscellaneous data:

1. Unloading and slaughter:

- a. Number of men used to take birds from coops\_\_\_\_\_
- b. Number of stickers (killers)\_\_\_\_\_
- c. Birds per minute per man\_\_\_\_\_
- d. Number of back up killers employed\_\_\_\_\_
- e. Average length of bleeding time (min,)\_\_\_\_\_

2. Scalding:

- a. Type of scalding\_\_\_\_\_
- b. Proportion of birds still struggling when entering  
scalding vat\_\_\_\_\_
- c. Temperature of scald water(F)\_\_\_\_\_
- d. Estimate of time in scalding (min.)\_\_\_\_\_
- e. Kind of additives used in scald water (if any)\_\_\_\_\_

3. Other information:

- a. Number of break downs in line during average working  
day\_\_\_\_\_
- b. Distance between shackles (in.)\_\_\_\_\_
- c. Are there separate cans for different types of  
condemned birds?  
1 yes \_\_\_\_\_  
0 no \_\_\_\_\_
- d. Are contaminated birds specially marked?  
1 yes \_\_\_\_\_  
0 no \_\_\_\_\_

## Appendix 3

Feed Utilization Procedure

-Volume of truncated cone was determined by taking measurements of the larger and smaller diameters and the side(s) of the cone, which were then used in the general equation for a truncated cone:

$$V = \frac{h}{3} (R_1^2 + R_1 R_2 + R_2^2)$$

Where:  $R_1$  is the larger diameter,

$R_2$  is the smaller diameter, and

$h$  is the vertical distance of the cone (See figure on the next page)

The volume of each right circular section on top of the cone was determined by measuring the distance between that distance by the number of rings. To derive the vertical distance of the section, the diameter of the section was taken from the larger diameter of the truncated cone. These measurements were then used in the general equation for a right circular cone,

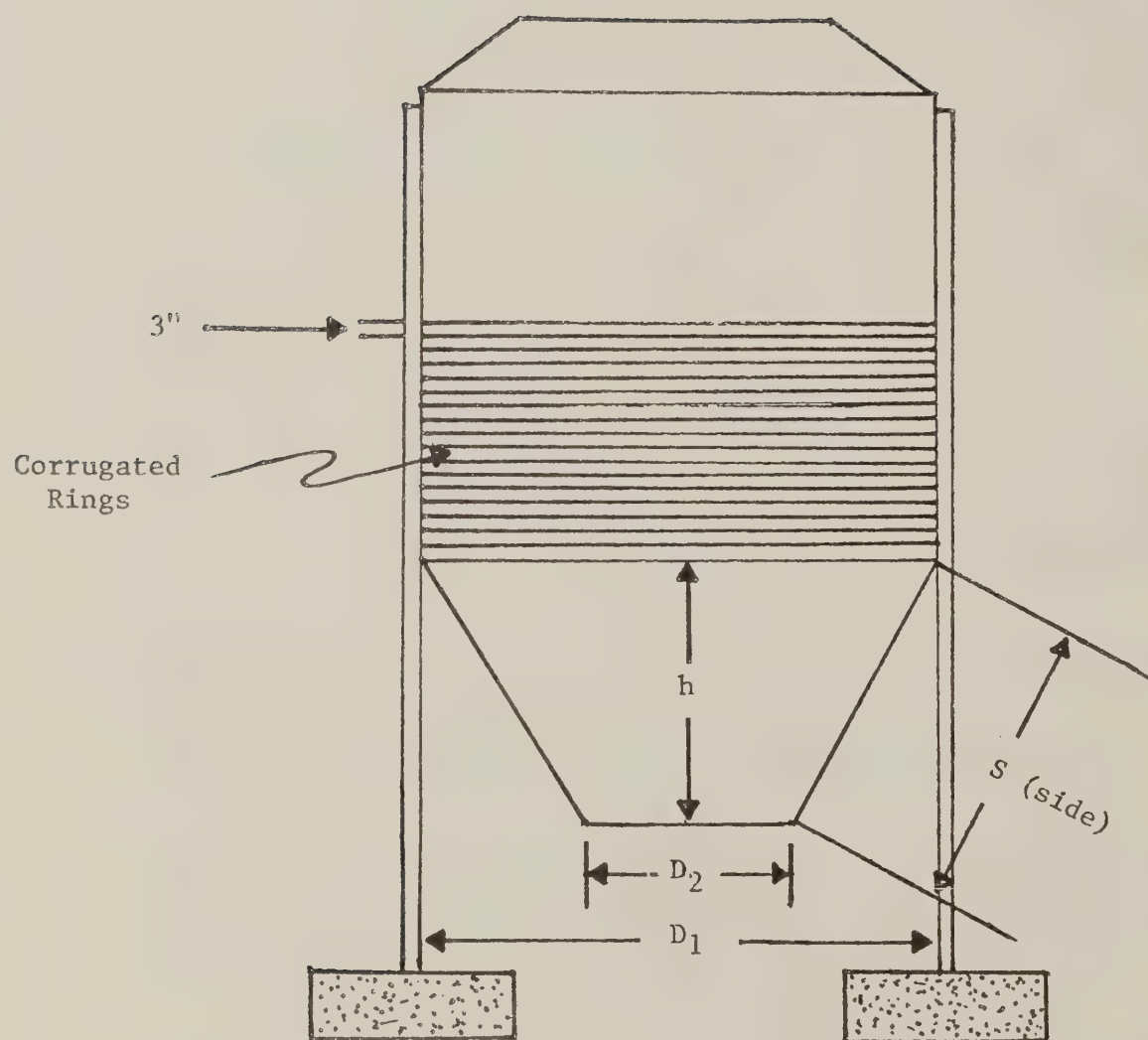
$$V = \frac{D^2}{4} h$$

Where:  $D$  is the diameter and

$h$  is the height of the section.

The volume of the section was multiplied by the number of sections. The total volume of the bin was taken to be the sum of the volume of the cone and the sections.

-To determine the weight of one cubic foot of feed, the



TYPICAL FEED BIN



total weight of the feed in the bin after it was filled (obtained from feed receipts), was divided by the total volume of the bin.

-To determine the amount of feed the birds consumed per week, the feed level in the bins was measured on a weekly basis. The level of feed was determined by hitting the side of the bins until the feed was leveled off. Based on the feed level, the volume of the left over feed was determined in the same manner as that of the method of calculating the volume of the bins. The weight of feed left in the bin was obtained by multiplying the volume of the left over feed by the weight of per cubic foot of feed. Therefore, the amount of feed consumed by a flock could be determined by subtracting the weight of feed left in the bin at a specific time from the total weight of feed placed in the bin. From the above procedure, the feed consumption of individual birds could also be calculated by dividing total feed utilized by the number of birds in the flock. This method provided the average amount of feed consumed per bird, per bin, per fill up.

#### Appendix 4

This appendix refers to all the computer printouts turned in to FSIS at the termination of the project.

## Appendix 5

Report of Bacteriologic Identification  
Poultry Disease Research  
School of Veterinary Medicine  
Tuskegee Institute

Source of Sample: Hatchery ( ) Poultry House ( )

Name of Company \_\_\_\_\_

Name of Hatchery \_\_\_\_\_

Name of Grower \_\_\_\_\_

Date of Original Sample Taken \_\_\_\_\_

Date of Identification Attempted \_\_\_\_\_

## I. Bacteria

Gram stain: Positive ( ) Negative ( )

Morphology: Rod ( ) Cocci ( )

## a. Blood agar

Colony morphology: Smooth ( ) Rough ( )

Size of colonies: Large ( ) Medium ( ) Small ( )

Hemolysis: Complete ( ) Viridan ( ) No ( )

## b. MaConkey agar

Colony morphology: Smooth ( ) Rough ( )

Size of colonies: Large ( ) Medium ( ) Small ( )

Color: Red ( ) Pink ( ) Colorless ( )

## c. Enterotube II. Yes ( ) No ( )

1. GLU ( ) GAS ( ) 2. LYS ( )

3. ORN ( ) 4. H<sub>2</sub>S ( ) IND ( )

5. ADON ( ) 6. LAC ( )

7. ARAB ( ) 8. SORB ( )

9. VP ( ) 10. DUL ( ) PA ( )

11. Urea ( ) 12. CIT ( )

## d. Others

Diagnosis:

## II. Fungus

a. Based on microscopic examination of morphology of culture.

Description:

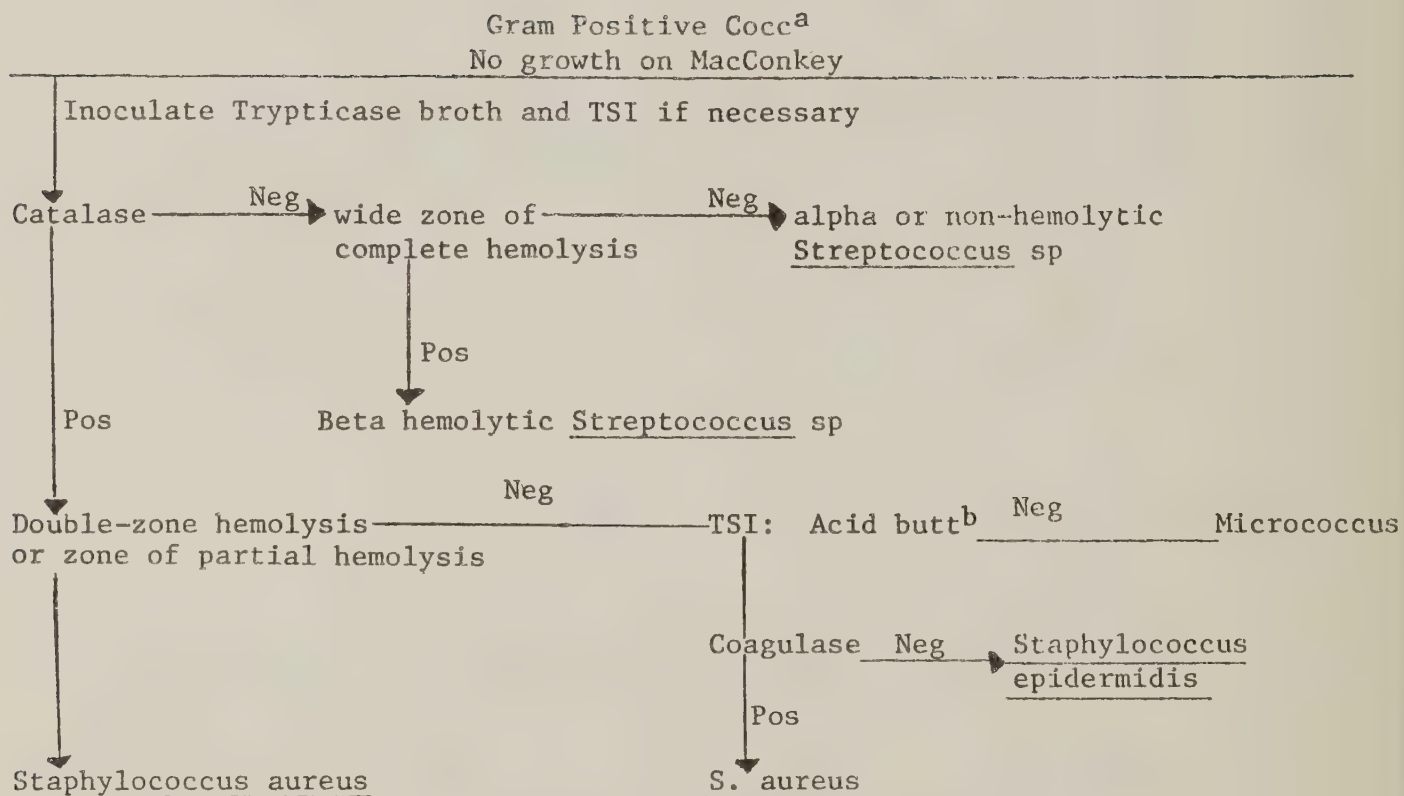
b. Colony color:

Diagnosis:

Diagnostician \_\_\_\_\_ Date \_\_\_\_\_

## FLOW CHART

## Appendix 5a



a) A broth culture can be gram stained to confirm morphology including chaining of Streptococcus.

b). TSI: The acid butt may be just turning yellow at 24 hours.

\*Source: John N. Berg. Diagnostic Veterinary Bacteriology Procedures and Species Identification. AAHA Annual Meeting Proceedings, 1979 (54).

# APPENDIX 5b MICROBIAL PROFILE

## DATA-FLOCK TESTING STUDY\*

STUDY FARM	POPULATION OF MICRO-ORGANISMS																								NECROPSY	CONDEMNATION RATE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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- \* B-Blood Agar M- McConkey Agar C- Corn Meal Agar
- \* Only 16 Observation with hatchery and corresponding farm data
- \* of these, 8 cases had TNTC or diffuse colonies
- \* Numbers in the blood agar and McConkey spaces refer to bacterial colonies.
- Numbers in the Corn Meal Agar spaces refer to fungal colonies



APPENDIX 5b MICROBIAL PROFILE (cont.)

DATA-FLOCK TESTING STUDY\*

STUDY FARM	POPULATION OF MICRO-ORGANISMS																	NECROPSY	CONDEMNATION RATE	
	HOUSE #																			
	HATCH			FARM			1			2			3			4				
	B	M	C	B	M	C	B	M	C	B	M	C	B	M	C	B	M			C
BROOD#																				
B-4	5	19	2	0			TNTC	.3	8	TNTC	2	TNTC	TNTC	1	8				--	0.312
B-5	3	65	37	0			45	1	0	199	1	0	-	-	-	-	-			
	5	106	40	3														2.010		0.239
B-6	3	6	2	4			340	.33	1	570	.33	1	1	-	-	-	-	--		0.226
B-7	3	26	-	.4			52	.33	1	477	1	2								
D-1	3						366	2	0	383	1	0	319	66	0	-	-	11.055		5.800
	4						TNTC	3	1	TNTC	1	2	TNTC	1	1			--		0.674
D-2	3						113	1	0	D	1	0	158	2	0	-	-	--		0.902
	4						TNTC	.1	3	TNTC	1	1	TNTC	3	6			--		0.579
D-3	3	2	1	1														--		1.023
D-4	4	22	9	0														--		0.618
D-5	4	28	3	1			28	3	3	TNTC	1	6						--		0.331
D-6	3	2	1	1														--		0.982
D-7	3						85	1	5	32	1	2						5.030		0.960
	4	38	1															--		0.868
E-1	2	3	1	0			D	1	0	-	-	-	-	-	-	-	-	1.508		0.686

\*D - Diffuse

APPENDIX 5b MICROBIAL PROFILE (cont.)

DATA-FLOCK TESTING STUDY\*

STUDY FARM		POPULATION OF MICRO-ORGANISMS																							NECROPSY	CONDEMNATION RATE	
		HOUSE #																									
		HATCH			FARM			1			2			3			4										
		B	M	C	B	M	C	B	M	C	B	M	C	B	M	C	B	M	C								
E-1	3	4	1	.2			TNTC	1	1																1.50	0.314	
	4	.5	0	.4			TNTC	19	7																	-	0.214
E-2	2						0	4	0																4.00	1.319	
E-3	2	4	1	.2			D	9	0	0	9	0	0	0	-	-	-	-	-	-	-	-	-	-	3.50	0.940	
	3						84	1	21	68	2	17													-	1.734	
	4						34	.1	1	48	1	.3													-	0.232	
E-4	2	3	1	0			D	.33	0	D	1	0	0	-	-	-	-	-	-	-	-	-	-	-	2.475	1.115	
	3						TNTC	1	3	57	.3	6													0.498	0.296	
E-5	2						770	15	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
E-6	2						14	0	1	29	0	0	0	-	-	-	-	-	-	-	-	-	-	-		1.209	
							43	.3	1	10	2	8													8.911	0.754	
E-7	2						D	1	25	D	0	6	6	D	0	9	D	0	9	D	0	9	D	0	9	3.50	0.380
F-1	2						34	1	.1																-	2.033	
	3						TNTC	15	TNTC																-	0.470	
F-2	1						TNTC	2	9	TNTC	1	TNTC													6.965	0.324	
F-2	3						TNTC	6	.1	TNTC	5	.1	TNTC	1	.1										-	0.283	

\*D- Diffuse

APPENDIX 5b MICROBIAL PROFILE (cont.)

DATA-FLOCK TESTING STUDY\*

STUDY FARM		POPULATION OF MICRO-ORGANISMS																								NECROPSY	CONDEMNATION RATE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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## Appendix 5c

Identification of Bacteria and Fungi Isolated  
From Hatcheries and Broiler Houses

CODE	ORGANISM	FREQUENCY
A-4	Micrococci sp	2
	Bacillus sp	1
	Staphylococci sp	2
	Cryptococci sp	2
	Moraxella sp. or Pasteurella sp.	
	or Pseudomonas sp. or Group 2K-1	
	Pseudomonas like or Alcaligene sp	1
	<u>Enterobacter agglomerans</u> or	
	<u>Shigella boydii</u>	
BP-B55	<u>Enterobacter agglomerans</u> or Citro-	
	bacter sp.	1
BP-B55	Micrococci sp	4
	<u>Proteus mirabilis</u>	
Ep-B45	Pseudomonas sp. or Alcaligenes sp	
	or Group M-4 Moraxella like	2
	<u>Salmonella enteritidis</u> bioses	
	para A or Citrobacter sp..	1
	<u>Pasteurella hemoltica</u>	1
	Listeria sp.	4
	2K-1Pseudomonas like	1
	Bacillus sp.	1
	<u>Enterobacter agglomerans</u>	1
	Non hemolytic streptococci	3
	Staphylococci sp	2
	<u>Corynebacterium pyogenes</u>	1
	Micrococci sp.	4
	Planococcus sp.	1
	Aerococci sp.	2
	Group A Pseudomonas like or	
	<u>Pseudomonas aeruginosa</u>	1
	<u>Escherichia coli</u> or <u>Klebsiella</u>	
	<u>ozanae</u>	2
	<u>Pseudomonas stutzeri</u>	2

Appendix 5c Identification of Bacterial and Fungi Isolated  
From Hatcheries and Broiler Houses (cont.)

CODE	ORGANISM	FREQUENCY
E-1	Enterobacter sp. or Citrobacter sp.	1
	Enterobacter sp	1
	Saccharomyces sp.	1
	Penicillium sp.	1
E-3	Micrococci sp	3
	Staphylococci sp.	3
	Bacillus sp.	1
	Aspergillus sp.	1
	Aspergillus sp.	1
	Penicillum sp.	1
E-6	Rhyzopus sp.	2
	Aspergillus sp.	1
	Penicillum sp.	1
EG - E65	<u>Pseudomonas cepacia</u>	1
	Listeria sp.	2
	Corynebacteria sp.	1
	Pseudomonas sp.	1
	Micrococci sp.	6
	Staphylococci sp.	4
	Penicillum sp.	1
	Penicillium sp.	1
F-1	Aspergillus sp.	1
	Trichosporon sp.	1
	Mucor sp.	1
F-2	Aspergillus sp.	2
	Penicillium sp.	2
FL	Penicillium sp.	1
DL - F45	Corynebacteria sp.	1
	Listeria sp.	2
	Bacillus sp	3
	Aerococci sp.	2
	Staphylococci sp	5



Appendix 5c Identification of Bacterial and Fungi Isolated  
From Hatcheries and Broiler Houses (cont.)

CODE	ORGANISM	FREQUENCY
F-2	Aerococci sp.	2
	Citrobacter sp.	1
	Alcaligenes or Group 2K-1	
	Pseudomonas like	1
	Citrobacter sp. or <u>Enterobacter</u>	
	<u>agglomerans</u>	1
	Pseudomonas sp.	1
	<u>Enterobacter agglomerans</u>	1
	<u>Shigella flexneri</u>	1
	Non-hemolytic streptococci	1
	Pseudomonas sp. or Alcalicines sp. or Group 2K-1 Pseudomonas like or Group M-4 Moraxella like	1
F-3	Staphylococci sp.	3
	Micrococci sp.	4
	Pseudomonas sp.	1
	pseudomonas sp.	1
	Streptococci sp. (alpha hemolytic)	1
	Streptococci sp. (Non hemolytic)	5
	Aerococci sp.	2
	<u>Escherichia coli</u>	1
	Moraxella-like Group M-4	1
	Enterobacter aerogenes or <u>Enterobacter cloacae</u>	1
	Enterobacter sp.	1
	Aspergillus sp.	1
	Cryptococcus sp.	1
	<u>Kloeckera apiculata</u>	1
	Aspergillus sp.	1

Appendix 5c Identification of Bacterial and Fungi Isolated  
From Hatcheries and Broiler Houses (cont.)

CODE	ORGANISM	FREQUENCY
	Group 5A Pseudomonas like or Pseudomonas aeruginosa	1
DL - D33/ D53/D63	Aspergillus sp.	1
DL - D14/ D24/D44	B-hemolytic streptococci	1
	Pennicillium	1
	Aspergillus sp.	1
DL - D54	Bacillus sp.	2
	Corynebacteria sp.	1
	Aspergillus sp.	1
	Pullularia sp.	1
D-5	<u>Pseudomonas cepacia</u>	1
	Listeria sp.	1
	Aspergillus sp.	1
D-6	<u>Pseudomonas cepacia</u>	1
	Listeria sp.	1
	Aspergillus sp.	1
E-1	<u>Escherichia coli</u>	1
	Pseudomonas sp.	1
	<u>Bordetella bionguiseptica</u>	1
	<u>Pseudomonas cepacia</u>	2
	<u>Pseudomonas aeruginosa</u>	1
	<u>Alcaligenes dinitrificans</u>	2
	Listeria sp.	1
	Cornebacteria sp.	1
	Klebsiella sp	1
	Providencia sp.	1
	<u>Enterobacter cloacae</u>	1
	<u>Acinetobacter luoffi</u>	1
	Staphylococcus sp.	1
	Aerococci sp.	1
	Micrococci sp.	1

Appendix 5c Identification of Bacterial and Fungi Isolated  
From Hatcheries and Broiler Houses (cont.)

CODE	ORGANISM	FREQUENCY
DL - F45	Micrococci sp	4
	Shigella sp.	2
	<u>Klebsiella pneumoniae</u>	1
	Alternaria sp.	1
	Penicillium sp.	1
DL - F55	Bacillus sp.	8
	Staphylococci sp.	5
	Micrococci sp.	6
	Alcaligenes sp. or Achromobacter sp.	1
	Listeria sp.	2
	Proteus sp.	1
	Non-hemolytic Streptococci sp.	7
	Corynebacteria sp.	2
	<u>Enterobacter agglomerans</u>	2
	<u>Alcaligenes dinitrificans</u>	1
	<u>Enterobacter cloacae</u>	2
	Pseudomonas sp. or Achromobacter sp.	1
	Aerococci sp.	1
	<u>Klebsiella pneumoniae</u>	1
	<u>Acinetobacter luoffi</u>	1
	<u>Pseudomonas stutzeri</u>	1
	Enterobacter sp. or Serratia sp.	1
F-1	Trichosporon sp.	1
	Micrococci sp.	3
	Staphylococci sp.	1
	Corynebacteria sp.	1
	Bacillus sp.	2
	Escherichia coli	2
	<u>Serratia liquefaciens</u>	1
F-2	Trichosporon sp.	1
	Bacillus sp.	2
	Staphylococci sp.	4
	Micrococci sp.	4

## Appendix 6

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
A-11	H-1	6		83.33	16.67			
A-31	H-1	6		100				
	H-2	6	83.33	16.67				
A-21	H-1	9	100					
A-41	H-1	6	83.3	16.67				
	H-2	6	33.33	33.33	16.67	16.67		
	H-3	6	16.67	33.33	33.33	16.67		
A-51	H-1	6	66.67	16.67			16.67	
A-61	H-1	6	66.67	16.67	16.67			
	H-2	6	50.0	33.33	16.67			
A-71	H-1	6	50.0	16.67	33.33			
	H-2	6	16.67	33.33	50.00			
A-12	H-1	10	30.0		30.0	30.0	10.0	
A-42	H-1	4	100					
	H-2	4	100					
	H-3	4	100					
A-52	H-1	4	100					
A-62	H-1	4	100					
	H-2	4	100					
A-72	H-1	4	100					
	H-2	4	100					
A-13	H-1	4	100					
A-23	H-1	4	100					
A-33	H-1	4	100					
	H-2	4	100					
A-43	H-1	4	100					
	H-2	4	100					
	H-3	4	100					
A-53	H-1	4	100					

## Appendix 6 (cont.)

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
A-63	H-1	4	100					0.621
	H-2	4	100					
A-73	H-1	4	100					0.460
	H-2	4		50.0	50.0			
A-14	H-1	4	50.0	50.0				0.938
A-24	H-1	4	100					0.573
A-34	H-1	4	100					0.377
	H-2	4	100					
A-44	H-1	4	100					0.494
	H-2	4	100					
	H-3	4	100					
A-35	H-1	4	100					0.691
	H-2	4	100					
A-45	H-1	4	100	50.0				1.020
	H-2	3	50.0					
	H-3	4	100					
	H-4	4	100					
B-11	H-1	5	20.0		80.0			0.255
	H-2	6			50.0	50.0		
B-21	H-1	16		62.50		37.50		0.138
	H-2	7	71.4		14.3	14.3		
B-31	H-1	10	40.0	40.0	20.0			0.212
B-51	H-1	12	41.7	25.0	33.33			0.232
	H-2	11	27.27	18.18	45.45	9.1		
B-12	H-1	8	50.0	50.0				0.221
B-22	H-1	10	100					0.171
B-32	H-1	4		25.0	50.0	25.0		0.543
B-42	H-1	4	100					0.288
	H-2	4	100					
	H-3	4	75.0	25.0				



## Appendix 6 (cont.)

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
B-52	H-1	4	100					0.259
	H-2	4	75.0	25.0				
B-62	H-1	4	100					0.084
	H-2	3		75.0	25.0			
B-13	H-1	4	100					0.231
	H-2	4	100					
B-23	H-1	4	100					0.344
	H-2	4	100					
B-43	H-1	4	100					0.137
	H-2	4	100					
	H-3	4	100					
B-53	H-1	4	100					0.239
	H-2	4	75.0		25.0			
B-73	H-1	4		100				-
	H-2	4		100				
B-14	H-1	4	50.0		25.0	25.0		0.367
	H-2	5				100		
B-24	H-1	4	100					0.243
	H-2	4	100					
B-44	H-1	4	100					0.211
	H-2	4	100					
	H-3	4	50.0	50.0				
B-54	H-1	4	100					0.248
	H-2	4	100					
B-64	H-1	4	100					0.114
	H-2	4	75.0	25.0				
B-15	H-1	4	100					0.368
	H-2	4			100			
B-45	H-1	4	100					0.312
	H-2	4	100					

## Appendix 6 (cont.)

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
B-65	H-1	4	100					0.218
	H-2	4	100					
D-11	H-1	6			100			0.934
	H-2	6	100					
	H-3		83.3	16.67				
D-21	H-1	6	100					0.714
	H-2	6	100					
	H-3	6	100					
D-31	H-1	6	100					1.037
	H-2	6		100				
	H-3	4		100				
D-41	H-1	6	66.67	33.33				0.658
	H-2	6	83.33	16.67				
	H-3	6	100					
D-12	H-1	4	100					0.662
	H-2	4	100					
	H-3	4	100					
D-22	H-1	4	75.0	25.0				1.177
	H-2	4	100					
	H-3	4	100					
D-32	H-1	4	100					2.703
	H-2	4	100					
	H-3	4	100					
D-42	H-1	4	100					1.207
	H-2	4	100					
	H-3	4	100					
D-52	H-1	8	75.0	25.0				0.401
	H-2	8	100					
D-62	H-1	4	100					0.477
	H-2	4	100					
	H-3	4	100					
	H-4	4	50.0		50.0			
D-72	H-1	4	50.0		50.0			0.817
	H-2	4	50.0		50.0			

## Appendix 6 (cont.)

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
D-13	H-1	4	100					5.800
	H-2	4	100					
	H-3	4	100					
D-23	H-1	4	100					0.902
	H-2	4	100					
	H-3	4	100					
D-33	H-1	4	100					1.023
	H-2	4	100					
	H-3	4	100					
D-43	H-1	4	100	25.0				1.002
	H-2	4	75.0					
	H-3	4	100					
D-53	H-1	4	75.0			25.0		0.865
	H-2	4	100					
D-63	H-1	4		100				0.982
	H-2	4		100				
	H-3	4	100					
	H-4	4	25.0		75.0			
D-73	H-1	4	75.0	25.0				0.960
	H-2	4	100					
D-14	H-1	4		25.0	50.0	25.0		0.674
	H-2	4			75.0	25.0		
	H-3	4	100					
D-24	H-1	4		25.0	50.0	25.0		0.579
	H-2	4	75.0		25.0			
	H-3	4	50.0	50.0				
D-64	H-1	4	100					0.449
	H-2	4	100					
	H-3	4	75.0	25.0				
	H-4	4	75.0	25.0				
D-74	H-1	4	100					0.868
	H-2	4	100					
D-55	H-1	4	100					0.478
	H-2	4	100					

## Appendix 6 (cont.)

BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
D-65	H-1	4	100		50.0		50.0	0.905
	H-2	4						
E-22	H-1	4	100					1.319
E-32	H-1	4	100	25.0				0.940
	H-2	4	75.0					
E-72	H-1	4	25.0	25.0	25.0	50.0	25.0	0.380
	H-2	4	25.0		50.0			
	H-3	4	25.0		50.0	25.0		
	H-4	4			75.0			
E-13	H-1	4	100					0.314
E-23	H-1	4	100					1.477
E-33	H-1	4		25.0	50.0	75.0		1.734
	H-2	4				50.0		
E-43	H-1	4	50.0	50.0				0.296
	H-2	4	75.0					
E-63	H-1	4	100					0.754
	H-2	4	1-0					
E-73	H-1	4	25.0	50.0	25.0	50.0		0.790
	H-2	4			25.0			
	H-3	4			75.0			
	H-4	4			50.0			
E-14	H-1	4	100					0.214
E-34	H-1	4	50.0	25.0	25.0			0.232
	H-2	4	100					
E-44	H-1	4	25.0	75.0	50.0			0.423
	H-2	4	25.0	25.0				
F-11	H-1	4		100				0.550
F-21	H-1	4	100					0.368
	H-2	4	100					
F-31	H-1	4	100					0.401
	H-2	4	100					

## Appendix 6 (cont.)

## BROILER SERA TITERS FOR NEWCASTLE DISEASE VIRUS AT FOUR WEEKS OF AGE

## Flock Testing Feasibility Study, Tuskegee Institute (1981/82)

CODE	HOUSE	TOTAL	NT	1:10	1:20	1:40	1:80	CONDEMNATION RATE
F-41	H-1	4	100					0.263
	H-2	4	100					
	H-3	4	100					
F-51	H-1	4	100					0.220
F-61	H-1	4	100					0.382
	H-2	4	100					
	H-3	4	100					
F-12	H-1	4	100					2.033
F-22	H-1	4		50.0	50.0			0.324
	H-2	4	100					
F-32	H-1	4	100					0.330
	H-2	4	100					
F-42	H-1		100					0.462
	H-2		100					
	H-3		100					
F-52	H-1		100					0.414
F-13	H-1		100					0.470
F-23	H-1		100					0.283
	H-2		100					
F-33	H-1		100					0.203
	H-2		100					
F-43	H-1		100					0.295
	H-2		100					
	H-3		100					
F-53	H-1			100				0.833



Pattern of disease (%) based on necropsy and Condemnation  
rate at slaughter for Flock Testing Study (1981-1982)\*

Appendix 7

STUDY UNIT	BROODS						$\bar{X}$	S.D.
	1	2	3	4	5			
Firm A Farm 1 Farm House 1	3(.649) "	.662(.648) "	(1.700) -	2.596(.983) "	(.747) "		.249 "	.138
Farm 2 Farm House 1	10.69(1.948) "	0(.508) "	1.005(.464) "	1.573 -	(.936)		.886	.622
Farm 3 Farm House 1 House 2	5.882(1.01) - -	.667(.542) - -	.503(.433) 0(.219) 1(.449)	.5(.377) - -	(.691)		.611	.250
Farm 4 Farm House 1 House 2 House 3 House 4	5.970(1.302) - - - -	.505(.463) - - - -	1.942(.425) 3.5(.45) 0(.252) 2.59(.284)	1.508(.494) 0 2.04(.62) 2 2	(1.020)		.741	.397
Farm 5 Farm House 1	19(.631) "	.662(1.417) "	(.280) -	(.529) -	(.603)		.692	.428
Farm 6 Farm House 1 House 2	3.15(.962) - -	.562(.450) - -	(.621) - -	(.742) - -	(.888)		.733	.206

\*Values in brackets are for condemnation rate (%), (figures outside brackets denote disease rate based on necropsy)  
 $\bar{X}$  - represents the mean of the respective rows or columns.

SD- represents the standard deviation of the respective rows and columns.

Appendix 7 (cont.) Pattern of disease (%) based on necropsy and condemnation rate at slaughter for Flock Testing Study (1981-1982)\*

STUDY UNIT	BROODS						$\bar{X}$	S.D.
	1	2	3	4	5			
Firm A Farm 7 Farm House 1 House 2	(.672) - -	0(.747) - -	(.460) - -	(.700) - -	(.701) - -		.656	.113
Firm B Farm 1 Farm House 1 House 2	1.818(.255) - -	1.316(.221) 2.29 0	3.0(.231) 1.25(.3) 4.16(.16)	(.367) - -	(.368) - -		.288	.073
Farm 2 Farm House 1 House 2	2.299(.138) - -	1.342(.171) - -	(.344) - -	(.243) - -	(.365) - -		.252	.101
Farm 3 Farm House 1	0(.212) "	3.106(.543) "	- -	- -	- -		.378	.234
Farm 4 Farm House 1 House 2 House 3	0(.204) - - -	2.22(.288) 0(.24) 1.64 7.77	3.98(.137) 2.97 5.77 4.16	4(.211) - - -	(.312) - - -		.230	.070
Farm 5 Farm House 1 House 2	.84(.232) - -	0(.259) - -	2.01(.239) - -	2.5(.248) - -	(.559) - -		.308	.141

Appendix 7 (cont.) Pattern of disease (%) based on necropsy and Condemnation rate at slaughter for Flock Testing Study (1981-1982)\*

STUDY UNIT	BROODS					$\bar{X}$	S.D.
	1	2	3	4	5		
Firm B Farm 6 House 1 House 2	3.614(.146) - -	.957(.084) - -	(.226) - -	1.5(.114) - -	(.218)	.158	.063
Farm 7 Farm House 1 House 2	2.655(.182) 4.8(.182) .81(.161)	.337(.282) 0(.315) .69(.249)	- - -	- - -		.232	.071
Firm D Farm 1 House 1 House 2 House 3	4.8(.934) - - -	0(.662) - - -	11.055(5.800) - - -	(.674) - - -	(.697)	1.753	2.265
Farm 2 Farm House 1 House 2 House 3	3.784(.714) - - -	0(1.177) - - -	(.902) - - -	(.579) - - -	(.730)	.820	.230
Farm 3 Farm House 1 House 2 House 3	3.0(1.037) - - -	4.975(2.703) - - -	(1.023) - - -	(.797) - - -	(.617)	1.235	.839

Appendix 7 (cont.) Pattern of disease (%) based on necropsy and Condemnation rate at slaughter for Flock Testing Study (1981-1982)\*

STUDY UNIT	BROODS						$\bar{X}$	S.D.
	1	2	3	4	5			
Firm D Farm 4 House 1 House 2 House 3	.529(.658) - - -	1.531(1.208) - - -	3.96(1.002) - - -	(.618) - - -	(1.222) - - -		.941	.291
Farm 5 Farm House 1 House 2	0(2.044) - -	.556(.401) - -	4.5(.865) - -	(.331) - -	(.478) - -		.824	.713
Farm 6 Farm House 1 House 2 House 3	0(.896) - - -	(.477) - - -	(.982) - - -	(.449) - - -	(.905) - - -		.742	.257
Farm 7 Farm House 1 House 2	.666(.488) - -	4.5(.817) - -	(.960) - -	(.868) - -			.783	.206
Firm E Farm 1 House 1	(.531) -	(.686) -	1.508(.314) "	1(.214) "			.441	.216
Farm 2 Farm House 1	(.601) -	(1.319) -	4(1.488) -	(.326) -	-		.931	.555

Appendix 7 (cont.) Pattern of disease (%) based on necropsy and condemnation rate at slaughter for Flock Testing Study (1981-1982)\*

STUDY UNIT	BROODS					$\bar{X}$	S.D.
	1	2	3	4	5		
Firm E Farm 3	(.780)	(.940)	4.5(1.734)	(.232)		.922	.621
House 1	-	-	3(.94)	-			
House 2	0	0	6(.941)	-			
Farm 4	(.444)	1.508(1.115)	2.48(.296)	.498(.423)		.570	.369
House 1	-	1.66(.602)	-	1(.31)			
House 2	-	1.26(.290)	-	0(.28)			
Farm 6	(1.892)	2.0(1.209)	(.754)	8.911		1.285	.573
House 1	-	1(1.72)	-	-			
House 2	-	3(2.16)	-	-			
Farm 7	(.387)	(0.380)	3(.790)	-		.519	.235
House 1	-	-	-	-			
House 2	-	-	-	-			
House 3	-	-	-	-			
House 4	-	-	-	-			
Firm F Farm 1	(.550)	(2.033)	1.1(.470)	-		1.018	.880
House 1	-	-	IV	-			
Farm 2	(.368)	(.324)	(.283)	6.95		.325	.043
House 1	-	-	-	5(.620)			
House 2	-	-	-	9			



Appendix 7 (cont.) Pattern of disease (%) based on necropsy and condemnation rate at slaughter for Flock Testing Study (1981-1982)\*

STUDY UNIT	BROODS					$\bar{X}$	S.D.
	1	2	3	4	5		
Firm F Farm 3 House 1 House 2	(.401) - -	(.330) - -	1.523(.202) 2.2(.33) .93(.44)	- - -		.311	.101
Farm 4 Farm House 1 House 2 House 3	(.263) - - -	(.412) - - -	1.493(.295) 0(.258) 2.8(.176) 1.3(.338)	2 3.3 0 2.5(.462)		.323	.078
Farm 5 Farm House 1	(.220) -	(.414) -	2(.836) "	.419 "		.490	.315
Farm 6 Farm House 1 House 2 House 3	(.382) - - -	(.321) - - -	2.488(.598) 1.47(.466) 4.54(.36) 2.24(.31)	- - - -		.434	.146

# APPENDIX -8 POSTMORTEM PROFILE OF BROILER SAMPLES\*

House Code	No. Birds Exam.	SEPTICEMIA-TOXEMIA			ALTRACULITIS			SYNOVITIS			SALPINGITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DERMATITIS			Total** Total Dis. Rate (House)	Total*** % Cond. (House)	**** USDA Cond. Rate	
		No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate	No. Dis- eased	Cond. Rate						
A11		100	2(2%)	2(2%)	1(1%)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3%	2	2%	0.649
A12		150	0	0	3(2%)	0	0	0	0	0	1(.67%)	1(.67%)	0	0	0	0	0	0	5	3.33%	1	.67%	0.648
A14		203	2(.99%)	2(.99%)	0	0	0	1(.49%)	0	0	1(.49%)	0	0	0	2(.99%)	2(.99%)	0	0	6	2.96%	3	1.48%	0.938
A21		159	2(1.26%)	2(1.26%)	13(8.18%)	1(1.26%)	0	0	0	0	0	0	0	0	0	0	0	0	15	9.43%	4	2.52%	1.948
A22		149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.508
A23		199	1(.50%)	1(.50%)	0	0	0	0	0	0	0	0	0	0	0	0	1(.50%)	0	2	1.01%	1	0.50%	0.464
A31		153	2(1.31%)	2(1.31%)	4(2.61%)	1(.65%)	0	0	0	0	0	0	0	0	2(1.31%)	1(.31%)	0	0	8	5.23%	5	3.27%	1.010
A32		150	0	0	1(.66%)	0	0	0	0	0	0	0	0	0	1(.66%)	1(.66%)	0	0	2	1.33%	1	0.67%	0.543
A32	1	99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.433
	2	100	0	0	0	0	0	0	0	0	0	1(0.5%)	0	0	0	0	0	0	1	0.5%	0	0	
A34	1	100	1(0.5%)	1(0.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.5%	1	0.5%	0.377
	2	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
A41		67	2(2.985%)	2(2.985%)	0	0	0	0	0	0	0	0	0	0	2(1.5%)	1(1.5%)	0	0	3	4.48%	23	2.985	1.302

\*Broiler samples were collected immediately after hock joints were cut.

\*\*Disease Rate - Any abnormalities caused by disease agent, regardless of severity, large percentage resulted in condemnation of diseased parts, some resulted in whole bird condemnation.

\*\*\*Condemnation - Opinion of the poultry pathologists in this project, following the criteria of USDA guidelines. Data only reflect whole bird condemnation.

\*\*\*\*USDA Condemnation Rate - Data furnished by USDA/FSIS on whole bird condemnation.

Note: Code represents the study farms (A,B,D, E,F), study farms (A1 -- F6) and brood cycles for each farm (1 - 5) Therefore, the alphabet only represents study farms, when coupled with one number e.g. A1, this represented a farm called A1, and when a third digit was added e.g. A22, the last digit represented the brood cycle.

## Appendix 8 (cont.) POSTMORTEM PROFILE OF BROILER SAMPLES (con't.)

House No.	No. Birds Exam.	SEPTICEMIA-TOXEMIA			AIRSACCULITIS			SYNOVITIS			SALPINGITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DEBRITIS			Total Dis. Rate (House)	Total No. Cond. (House)	Total % Cond. (House)	USDA Cond. Rate
		No. Dis- eased	No. Dis- Rate	Cond. Rate	No. Dis- eased	No. Dis- Rate	Cond. Rate	No. Dis- eased	No. Dis- Rate	Cond. Rate	No. Dis- eased	No. Dis- Rate	Cond. Rate	No. Dis- eased	No. Dis- Rate	Cond. Rate	No. Dis- eased	No. Dis- Rate	Cond. Rate				
A42	1	60	1 (0.5%)	1 (0.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.5	0.288	
	2	88	0	0	1 (0.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
	3	52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
A43	1	57	0	0	2 (0.97%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.97%	0	0.425
	2	72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2 (.97%)	0	0	2	0.97%	0	0
	3	77	1 (.49%)	1 (.49%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.49%	1	0
A44	1	50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.494	
	2	49	1 (.50%)	1 (.50%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.50%	1	0
	3	50	0	0	1 (.50%)	1 (.50%)	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1.01%	1	0
	4	50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.50%	0	0
A51		111	0	0	1 (.90%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.90%	0	0.631
A52		151	0	0	7 (4.64%)	3 (1.99%)	0	0	0	0	0	0	0	0	0	0	0	0	0	7	4.64%	3	1.417
A61		127	2 (1.5%)	2 (1.5%)	1 (.79%)	0	0	0	0	0	0	0	0	1 (.79%)	1 (.79%)	0	1 (.79%)	0	0	5	3.94%	3	0.962
A62	1	100	0	0	1 (1%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1%	0	0.450
	2	100	1 (1%)	1 (1%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1%	1	0









## Appendix 8 (cont.)

## POSTMORTEM PROFILE OF BROILER SAMPLES (cont.)

House Code	No. Birds Exam.	SEPTICEMIA-TOXEMIA			AIRSACCUULITIS			SYNOVITIS			SALPINGITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DERMITITIS			Total No. Cond. (House)	Total % Cond. (House)	USDA Cond. Rate	
		No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate				
B71	103	2(1.94%)	2(1.94%)	94%	3(2.9%)	0	0	0	0	0	0	0	0	0	0	0	0	0	5	4.85%	2	1.94%	0.182
	123	2(1.63%)	2(1.63%)	63%	0	0	0	0	0	0	0	0	0	0	0	2(1.63%)	0	0	4	3.25%	1	0.81%	0
B72	150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.282	
	147	1(.68%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.68%	1	0.68%	0
B61	33	0	0	0	3(3.61%)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3.61%	1	1.2%	0.146
	111	1(.49%)	1(.49%)	1(.49%)	2(.99%)	0	0	0	0	0	0	0	0	0	0	1(.49%)	0	0	4	1.99%	2	0.99%	0.450
B62	2	0	0	0	1(.49%)	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.49%	0	0	0
	200	0	0	0	2(1%)	0	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	3	1.5%	0	0	0.114
B11	125	2(1.6%)	2(1.6%)	2(1.6%)	4(3.2%)	1(.8%)	0	0	0	0	0	0	0	0	0	0	0	0	6	4.8%	2	1.6%	0.934
	78	0	0	0	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.5%	0	0	0.662
B12	2	0	0	0	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.5%	0	0	0
	42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B13	199	1(.50%)	0	0	2(0.55%)	0	0	0	0	0	0	0	0	0	0	0	0	0	22	11.06%	7	3.52%	5.800
	185	2(1.08%)	2(1.08%)	0.8%	5(2.72%)	1(.54%)	0	0	0	0	0	0	0	0	0	0	0	0	7	3.78%	3	1.62%	0.714

Appendix 8 (cont.)

POSTMORTEM PROFILE OF BROILER SAMPLES (cont.)

Code	House No.	No. Birds Exam.	SEPTICEMIA-TOXEMIA			AIRSACCUITIS			SYNOVITIS			SALPINGITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DERMITITIS			Total No. Cond. (House)	Total % Cond. (House)	USDA Cond. Rate
			No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate	No. Dis- eased	No. Cond. Rate			
D22	1	80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.49%	1.177
	2	62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1.28%	0.8
	3	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.49%	0
D31		132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.037
D32		201	1(.49)	1(.49)	13(6.47%)	4(1.99%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2.49%	2.703
D41		189	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.658
D42		200	1(.5%)	1(.5%)	3(1.5%)	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1%	1.207
D43		202	0	0	4(1.98%)	2(.99%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.99%	1.002
D51		98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.044
D52		200	1(.5%)	1(.5%)	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1%	0.401
D53		200	1(.5%)	1(.5%)	5(2.5%)	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1%	0.865
D61		92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.896
D71		150	0	0	1(.67%)	1(.67%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.67%	0.488

## Appendix 8 (cont.)

## POSTMORTEM PROFILE OF BROILER SAMPLES (con't.)

House Code	No. Birds Exam.	SEPTICEMIA-TOXEMIA			AIRSACCUITIS			SYNOVITIS			SALPINCITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DERMITITIS			Total No. Cond. (House)	Total % Cond. (House)	USDA Cond. Rate	
		No. Dis-eased	Cond. Rate	Cond. Rate	No. Dis-eased	Cond. Rate	Cond. Rate	No. Dis-eased	Cond. Rate	Cond. Rate	No. Dis-eased	Cond. Rate	Cond. Rate	No. Dis-eased	Cond. Rate	Cond. Rate	No. Dis-eased	Cond. Rate	Cond. Rate				
D72	200	1(.5%)	1(.5%)	8(4%)	2(1%)	0	0	0	1(.5%)	0	0	0	0	0	0	0	0	0	10	5%	3	1.5%	0.819
D73	199	0	0	9(4.523%)	2(1%)	0	0	0	0	0	0	0	0	0	0	0	1(.5%)	0	10	5.03%	2	1.01%	0.960
E12	201	0	0	1(.498%)	1(.498%)	0	0	0	1(.498%)	0	0	0	0	0	0	0	1(.498%)	0	3	1.493%	1	0.498%	0.686
E13	200	0	0	3(1.5%)	1(0.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1.5%	1	0.5%	0.314
E22	200	1(0.5%)	1(0.5%)	5(2.5%)	0	0	0	0	0	0	0	0	0	0	0	0	2(1%)	0	8	4.0%	1	0.5%	1.319
E32	100	1(0.5%)	1(0.5%)	1(0.5%)	0	0	0	0	0	0	0	0	0	0	0	0	1(0.5%)	0	3	3.0%	1	1.0%	0.940
E41	199	1(.50%)	1(.50%)	1(.50%)	0	0	0	0	1(.50%)	0	0	0	0	0	0	0	1(.50%)	0	4	2.01%	1	0.50%	0.444
E42	202	1(.495%)	1(.495%)	1(.495%)	0	0	0	0	1(.495%)	0	0	0	0	0	0	0	2(.99%)	1(.495%)	5	2.475%	2	0.99%	1.115
E43	1	0	0	1(.498%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.498%	0	0	0.296
E61	200	2(1%)	2(1%)	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	3(1.5%)	1(.5%)	6	3.0%	3	1.5%	1.892
E63	1	2(.95%)	2(.95%)	7(3.467%)	2(.99%)	0	0	0	0	0	0	0	0	0	0	0	0	0	11	5.446%	4	1.980%	0.754
2	100	1(.495%)	1(.495%)	6(2.970%)	1(.495%)	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3.465%	2	0.99%	
E72	200	2(1%)	2(1%)	4(2%)	0	0	0	0	0	0	0	0	0	0	0	0	1(1%)	1(1%)	7	3.5%	3	1.5%	0.380

## Appendix 8 (cont.) POSTMORTEM PROFILE OF BROILER SAMPLES (con't.)

Code	House No.	No. Birds Exam.	SEPTICEMIA-TOXEMIA			AIRSACCUULITIS			SYNOVITIS			SALPINCITIS			SQUAMOUS CELL CARCINOMA			NECROTIC DERMITITIS			Total Dis. Rate (House)	Total No. Cond.	Total % Cond. (House)	USDA Cond. Rate
			No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate	No. Dis-eased	No. Cond.	Rate				
F21		181	1(.55%)	0	1(.55%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0.55%	0.550	
F22	1	100	1(.498%)	1	1(.498%)	1(.498%)	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	0.995%	0.324	
	2	101	1(.498%)	1(.498%)	1(.498%)	1(.498%)	0	0	0	0	0	0	0	0	0	0	0	0	0	9	2	0.995%	0	
F31	1	107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.401	
	2	90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0.508%	0	
F32	1	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.330	
	2	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0.5%	0	
F41	1	54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.263	
	2	71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
	3	76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
F42	1	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
	2	80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0.412	
	3	60	1(.5%)	1(.5%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0.5%	0	
F51		200	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.220	
F52		203	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.414	
F61		201	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	0.995%	0.382	



APPENDIX 9 INITIAL VARIABLES USED FOR DEVELOPING A PREDICTIVE MODEL FOR  
POULTRY CARCASS CONDEMNATION RATES IN PROCESSING PLANTS.

VARIABLE CODEVARIABLE DEFINITION

ID	Firm/Farm/Brood Code
X57	Hatchery Source #1
X58	Hatchery Source #2
X59	Hatchery Source #5
X260	Hatchery Source #4
X261	Hatchery Source #5
X262	Hatchery Source #6
X263	Hatchery Source #7
X60	Incubator Type #1
X61	Incubator Type #2
X62	Average Fertility Rate (%) For Hatchery
X63	Average Hatchability Rate (%) For Hatchery
X64	Average Fertility Rate (%) For Brood of Birds
X65	Average Hatchability Rate (%) For Brood of Birds
X66	Number Of Days Eggs Held On Farm
X67	Number Of Days Eggs Held In Hatchery
X69	Number Of Breeder Flocks Supplying Eggs for Hatchery
X264	Location Of Air Intakes In Hatchery (Roof)
X78	Location Of Air Intakes In Hatchery: East, North East
X79	Location Of Air Intakes In Hatchery: North, North West
X80	Location Of Air Intakes In Hatchery: West, South West
X265	Location Of Air Exhaust From Hatchery (Roof)
X81	Location Of Air Exhaust From Hatchery: East, North East
X82	Location Of Air Exhaust From Hatchery: North, North West
X83	Location Of Air Exhaust From Hatchery: West, South West
X84	Date Of Setting Of Eggs For Brood (Calendar Day Starting at Jan. 1)
X3	Total Number Of Birds In (Farm/House)
X221	Number of Birds Shipped From Farm For Processing
X222	Average Slaughter Weight On Date Of Marketing (lbs.)
X7	Proportion (%) Of Undersized Birds
X8	Strain Group 1
X9	Strain Group 2
X10	Strain Group 3
X14	Total Number Of Strains On Farm
X15	Total Number Of Breeder Flock Sources For Farm
X16	House Type 1
X17	House Type 2
X18	Average Population Density Per Square Feet
X19	Average Distance Between Houses On Farm
X20	Ventilator Type 1
X22	Number Of Ventilators
X23	Location Of Air Intakes In Broiler House: East, North East
X24	Location Of Air Intakes In Broiler House: North, North West
X25	Location Of Air Intakes In Broiler House: West, South West
Z5	Location of Air Intakes In Broiler House: South, South East



## APPENDIX 9 (cont.)

<u>VARIABLE CODE</u>	<u>VARIABLE DEFINITION</u>
X26	Location Of Air Exhausts In Broiler House: East, North East
X27	Location Of Air Exhausts In Broiler House: North, North West
X28	Location Of Air Exhausts In Broiler House: West, South West
Z6	Location of Air Exhausts in Broiler House: South, South East
X39	Age Specific Mortality Rate (%) At 4 Weeks
X40	Age Specific Mortality Rate (%) At 7 Weeks
X85	Date Of Placing Of Chicks For Brood Starting Jan. 1
X87	Length Of Time For Preheating (Hours)
X88	Brooding Type
X89	Length of Stay Of Birds In Broiler House (Day)
X90	Age Broiler Guards Removed (Day)
X91	Number Of Chicks Per Broiler Hours (Average)
X109	Average Disease Rate (%) Based On Necropay At 7 Weeks
X110	Disease Specific Rate (%) Based on Necropsy (1 = Leucosis)
X111	Disease Specific Rate (%) Based On Necropsy (2 = Septicemia-Toxemia)
X112	Disease Specific Rate (%) Based On Necropsy (3 = Airsacculitis)
X113	Disease Specific Rate (%) Based On Necropsy (4 = Synovitis)
X114	Disease Specific Rate (%) Based On Necropsy (5 = Tumors)
X115	Disease specific Rate (%) Based On Necropsy (6 = Others)
X116	Mash (Type Of Feed)
X117	Crumbles (Type Of Feed)
X119	Feeder Space Per Bird
X121	Feed Spillage (Present Or Not)
X122	Feed Source #1
X123	Feed Source #2
X124	Feed Source #3
X266	Feed Source #4
X125	Number of Feed Deliveries Per Month
X127	Number of Waterers Used During Brooding
X129	Water Spacing Per Bird
X130	Age Manual Waterers Removed (Days)
X131	Water Spillage (Present Or Not)
X132	Average Feed Utilization Rate For (Farm/House) At 4 Weeks
X133	Average Feed Utilization Rate At 7 Weeks
X148	Duration Of Prophylactic Medications (Days)
X165	Growth Promoters Only
X169	Vaccine Manufacturers #1
X170	Vaccine Manufacturers #2
X171	Vaccine Manufacturers #3
X186	Farm Sanitation Index
X189	Litter Type 1
X267	Litter Type 2
X190	Depth Of Litter (Inches)
X194	Nubmer of Batches In Litter
X202	Average Maximum Temperature For Study Blood (F)
X203	Average Temperature For Study Brood (F)

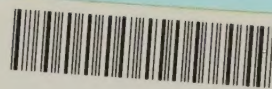
VARIABLE CODEVARIABLE DEFINITION

X204	Average Minimum Temperature For Study Brood (F)
X205	Average Total Precipitation For Study Brood (Inches)
ZR	Number Of Rainy Days
X206	Fall (Season Brood Of Birds Raised)
X207	Winter
X208	Spring
X223	Distance From Farm To Plant (Miles)
X224	Number Of Hours of Driving From Farm To Plant
X226	Number Of Different Drivers Involved In Flock Delivery
X227	Number Of Trips To Haul Whole Flock To Plant
X228	Number Of Trucks Used To Transport Birds
X230	Number Of Birds Per Coop
X231	Number Of Birds Per Truck
X235	Number Of Birds Dead On Arrival At Plant
X237	Number Of Days Involved In Marketing Flock
X241	Number Of Inspectors On Line
X245	Semi-Traditional Inspection
X247	Processing Plant #1
X248	Processing Plant #2
X249	Processing Plant #3
X250	Processing Plant #4
X251	Daily Total Capacity Of Processing Plant
X252	Number Processed For Entire Day
X253	Total Number Of Employees In Plant
X254	Number Of Hours Per Day Plant Operates
X255	Number Of Shifts
Y1	Average Condemnation Rate (%) Due To Diseases For Processing Plant
Y2	Condemnation Rate (%) Due To Diseases For Study Farm
Y3	Disease Specific Condemnation Rate (%) For All Farms (1 = Leucosis)
Y4	Disease specific Condemnation Rate (%) For All Farms (2 = Septicemia-Toxemia)
Y5	Disease Specific Condemnation Rate (%) For All Farms (3 = Airsacculitis)
Y6	Disease Specific Rate (%) For All Farms (4 = Synovitis)
Y7	Disease Specific Rate (%) For All Farms (5 = Tumors)
Y8	Disease Specific Rate (%) For All Farms (6 = Others)
Y9	Disease Specific Condemnation Rate (%) For Study Farm (1 = Leucosis)
Y10	Disease Specific Condemnation Rate (%) For Study Farm (2 = Septicemia-Toxemia)
Y11	Disease Specific Condemnation Rate (%) For Study Farm (3 = Airsacculitis)
Y12	Disease Specific Condemnation Rate (%) For Study Farm (4 = Synovitis)
Y13	Disease Specific Condemnation Rate (%) For Study Farm (5 = Tumors)
Y14	Disease Specific Condemnation Rate (%) For Study Farm (6 = Others)
Y15	Overall Condemnation Rate (%) Due To Diseases For Study Farm
Y16	Average Condemnation Rate (%) Due To Non-Diseases For Processing Plant
Y17	Condemnation Rate (%) Due To Non-Diseases For Study Farm
Y2T	Previous Condemnation Rate (%) Due To Diseases For Study Farm



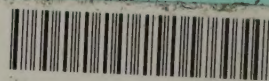
## Appendix 9 (cont.)

<u>VARIABLE CODE</u>	<u>VARIABLE DEFINITION</u>
Y9T	Disease Specific Condemnation Rate (%) of previous brood For Study Farm (1 = Leucosis)
Y10T	Disease Specific Condemnation Rate (%) of previous brood For Study Farm (2 = Septicemia-Toxemia)
Y11T	Disease Specific Condemnation Rate (%) of previous brood For study Farm (3 = Airsacculitis)
Y12T	Disease Specific Condemnation Rate (%) of previous brood For study Farm (4 = Synovitis)
Y13T	Disease Specific Condemnation Rate (%) of previous brood For Study Farm (5 = Tumors)
T14T	Disease Specific Condemnation Rate (%) of pervious brood For Study Farm (6 = Others)



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